Title:

Searched:

Database

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1 atgaagtatttcttgatttc.....atgaagttgatgaagattaa 375
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Listing first 45 summaries
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                                          RESULT 1
AX036541
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 38 42.6 11.4<br>39 42.4 11.3<br>40 42.4 11.3<br>41 42.4 11.3<br>42 42.4 11.3<br>42 42.4 11.3<br>43 42.4 11.3<br>44 42.4 11.3<br>45 42.2 11.3             | 43.4 11.6<br>43.4 11.6<br>43.2 11.5<br>43.2 11.5<br>43.2 11.5<br>43.3 11.5<br>43.8 11.5<br>42.6 11.4                           | 20 44.4 11.8<br>22 44.4 11.8<br>22 44.2 11.8<br>24 43.6 11.6<br>25 43.6 11.6<br>26 43.6 11.6<br>27 43.6 11.5  | 5.2 12.1 22<br>5.2 12.1 23<br>5.2 12.1 13<br>5.2 12.1 13<br>5.2 12.1 13<br>5.2 12.1 13<br>5.2 12.1 16<br>6.2 11.9 12<br>6.4 11.8 6<br>7.4 | 375 100.0 18 48.6 13.0 18 48.6 13.0 20 46.4 12.4 29 45.8 12.2 4 45.8 12.2 4                         | re Ma       |
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| AC096326 Rattus no AF093702 Plasmodiu AC131380 Strongylo AC104634 Homo sapi AC102659 Mus muscu AL773546 Mus muscu AL7735475 Plasmodiu AJ296740 Picea abi | B Danio Ra<br>B Danio sa<br>C Homo sa<br>71 T7 end<br>5 Homo sa<br>ation (2<br>1 Rattus<br>9 Homo sa<br>9 Homo sa<br>3 Homo sa | ACO27820 Homo sapi<br>ACO91153 Homo sapi<br>ACO911593 Mus muscu<br>Continuation (2 of<br>ALO31744 Plasmodiu<br>AL807765 Mus muscu<br>AL711007 Mus muscu | mus<br>ophi<br>ophi<br>ophi<br>ophi<br>ophi<br>sap<br>sap   | Seq<br>Mus<br>Cae<br>Cae<br>Cae<br>Seq<br>Seq<br>Hom  | Description |

TITLE Hirudo medicinalis

Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

1 (bases 1 to 375)

Hemberger, J., Scheuble, B., Strittmatter, W., Hofmann, U., Fotev, Z. 375 bp Sequence 1 from Patent W00056885. AX036541 medicinal leech. Protein for blocking platelet adhesion and Guessow, D AX036541.1 GI:11226151 JAWK SAWK

ALIGNMENTS

DNA

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PAT 16-NOV-2000

Pred. No.

is the number of results predicted by chance to have

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us-09-936-737a-1.rge

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                         Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 19, 2002 this sequence version replaced gi:21738804.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                    HTG;
      Center:
                                                                           Submitted (16-JUL-2002) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                     SnW
                                                                                                     Direct Submission
                                                                                                                                                                                  Mus musculus
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HEMBERGER JUERGEN (DE); MERCK PATENT GMBH (DE); SCHEUBLE BERNHARD (DE); STRITMATTER WOLFGANG (DE); HOFMANN UWE (DE); FOTEV ZISI (DE); GUESSOW DETLEF (DE)
                                                                                                                                    (bases 1 to 189967)
                                                                                                                                                                                                musculus.
                                                                                                                                                                                                                                                             musculus chromosome 4 clone RP23-17A4, ***
SRESS ***, 13 unordered pieces.
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Wellcome Trust Sanger Institute
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/db_xref="taxon:6421"
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Consensus quality: 186623 bases at least Q40
Consensus quality: 187480 bases at least Q30
Consensus quality: 188086 bases at least Q20
Insert size: 188767; sum-of-contigs
Insert size: 215919; 10.9% error; agarose-fp
Quality coverage: 5.28x in Q20 bases; sum-of-contigs Quality
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8455 8554: gap of 100 bp
19308 19407: gap of 10753 bp in length
19308 27997: contig of 7690 bp in length
27098 27197: gap of 100 bp
27198 40822: contig of 3625 bp in length
40823 40922: gap of 100 bp
40823 40922: gap of 100 bp
40824 40861: gap of 100 bp
48862 94932: contig of 7839 bp in length
48862 94932: contig of 46071 bp in length
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130870 146267: cont
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146368 151984; contig of 5617 bp
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/note="assembly_fragment:00793
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146267: contig of 15398 i
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gap of 100 bp
2: contig of 32028 bp in lengtn
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100 bp in length.
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                                                                                                                                                                                                                                                                                          sequence.
                                                                                                                                                                                                                                                                                                            Mouse DNA sequence from clone RP23-207H16 on chromosome 4, complete
                              Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Aug 23, 2002 this sequence version replaced gi:21690116.
                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Center: Wellcome Trust Sanger Institute
                                                                                           Direct Submission
Submitted (22-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
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                     -- Genome Center
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ORGANISM
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Best Local Similarity 48.4%;
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Only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by at least as compressions and repeats; all regions were covered by at least as compressions and repeats; all regions were covered by at least as compressions are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviation of the workper in the feature table with their source databases: Em. EMBL; Sw:, in the feature table with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-207H16 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                         Caenorhabditis elegans Caenorhabditis elegans
                                                                                                                                                                                                                                                       Caenorhabditis elegans cosmid C30F8, complete sequence
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis
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REFERENCE

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                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
The 5' cosmid is C46H11, 8300 bp overlap; the 3' cosmid is Y110A7A,
                                                                                                                                         For a graphical representation of this cosmid sequence and its
                                                                                            www.wormbase.org/db/seq/sequence?name=C30F8;class=Sequence
                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                           neighboring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-APR-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-FEB-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-AUG-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (Ol-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (23-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Latrell, P., Twyman, B. and Wilson, R.
The seguence of C. elegans cosmid C30F8
Unpublished (2001)
(bases 1 to 40090)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9851916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRO, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63110, USA
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                                                         NEIGHBORING COSMID INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l to 40090)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            st.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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(http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae 10:115-1125, 2000), individual C. elegans Genome Research and personal communications with C. elegans GenBank submissions, are predicted using the program trNAscan's (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coding seqences below are the result of integration and manual review of the following data : computer analysis using the program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genefinder (P. Green and L. Hillier, personal communication), the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200\, bp overlap. Actual start of this cosmid is at base position 197 of C30F8; actual end is at 40090 of C30F8.
/product="Hypothetical
/protein_id="AAK85457.1
/db_xref="GI:15150650"
                                                                                                                                   /notee similar to protein kinases (PFam; pkinase, score; 183.25); coded for by the following C. elegans cDNAs: yk739d9.5, yk284c11.3, yk284c11.5, yk465a7.5, yk739d9.3, yk649h5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Hypothetical protein C30F8.2"

/product="G1"-NAK85455.2"

/db_xref="G1:16259229"

/translation="MGEFLFNIDHGYLEALTRGLKGGLLAQADYANLYQCETLEDLKLHIQSTDYGNFLANEPGATTYQVUDEKLKEKLYTEFTHLRNNALEPLATFLDYITYSYM
HIQSTDYGNFLANEPGATTYQVUDEKLKEKLYTEFTHLRNNALEPLATFLDYITYSYM
LDNIILLITGTLHQRPISELINKCHPLGSFEQMEAIHLASTPAELYNAVLYDTPLANY
FYDCINEQDLDEMNYEVIRNILYKAYIEDFYKFCAGLGGKTAEVMCDILAFEADRRSI
ITTINSFDTELSKDDRQKLYPRCGKLFPDGLTGLSRADDYDQVKQVCEFYSDYKPLFE
                                                                                                                                                                                                                                                                join(25607. .25684,27245. .27344,27393. .2
28346. .28436,28489. .28707,28818. .29897,
30070. .30315,32038. .32325,32760. .32891)
/gene="C30F8.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(21528. .21529)
/note="SL1 trans-splice site; see yk821a09.3"
complement(21534. .21535)
/note="SL1 trans-splice site; see yk809d10.5"
25607. .32891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="coded for by the following C. elegans cDNAs: yk71032.3, yk449d2.3, yk705g11.3, yk745d7.3, yk169b6.3, yk809d10.3, yk807a04.3, yk702g3.3, yk105h9.3, yk105h9.5, yk169b6.5, yk306e11.5, yk43ff1.3, yk43lf1.5, yk449d2.5, yk479e6.5, yk859d05.5, yk710g2.5, yk702g3.5, yk888h07.5, yk745d7.5, yk763e04.5, yk821a09.5, yk809d10.5, yk754e11.3, yk888h07.3, yk773c05.3, yk821a09.3°
                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                        [www.wormbase.org/db/seq/sequence?name=C30F8.4a;class=Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="for a graphical representation of this gene see:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="C30F8.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGNGPGEKTLEDKFFEHEVKLNVHSYLHQFHFGVFYAFIKLKEQEMRNIIWIAECIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(19565. 20460. .20617,20879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {www.wormbase.org/db/seq/sequence?name=C30F8.2;class=Seque
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/strain="Bristol N2"
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20879. .21057,21102. .21273,21392. .
                           u protein C30F8.4a"
                                                                                                                                                                                                                                                                                                          29897,29946. .30020,
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CDS

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DEFINITION
                                  ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8523 TTTCTCTTTTTTCAATACATTTCCTACAAATTTTGAGGCTTCTGACTTGCTCTAAAAAA 8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                            8643 TTTGGAGAATTTTCTTATTCTGAAAAATCCTTACCAAAATAATTTCAGATTGTTTTTTC 8702
                                                                                                                                                                                                                                                                                                                      8703 AAAAAATTTTTT 8714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 TTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGC 186
                                                                                                                                                                                                                                                                                                                                                                                           187 TACATCGTTTTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101; Conservative
                                             AC006845.1 GI:4263503
                                      AC006845
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ADFGLSRALDVDAVYTASRGKLPIKWLAPESVNYROPSMASDVMMFGYCMWEIFSLGV
KPWAGYTNSDVIMHIROGSRPPCPEKCPTALYNEIRSKMWAIEPHKRPTVDQIYAIIE
DYRQQIIONIPPEQIIYGKENGYLWAEMSSLPGJTLYKRTMEDQKKQAEEDAKWLE
DYRQDIIOQIPPEQIIYGKOMYAAGSLPGJTLYKRTMEDQKKQAEEDAKWLE
OEDDEDDEDDIDQIIQIPSTSHSSVENIRTSNGYLHHTPTSTRSLKFEDKTSRGLKRSVD
OEDDEDDEDDIQIIQFTSHSSVENIRTSNGYLHHTPTSTRSLKFEDKTSRGLKRSVD
OKUDAYTKLONGFNNLTHNDDFLHSVKEVTSQLREMLIVASGMKDRVTTTTQRTDVDM
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HFALKLYTGPSPQTAGSGDSLWLHPMLRITQLPHIYARHLPIGVCDEIKLEMRWREMP
OSVYELQATDSSAFYYLHEQVVDEFFSHVAWRSSYEVALEVAALKVCRDFAEHQHNKG
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IERCETLIMHEATIRPKTPNNIDSNIRLRRELITLKELIGGGQFGNVYKAVYHDLEKD
ERIAVAVKVCKTDAEPADTOLILQESSLMRNFRHSNIIQLIGVCVDQPMWLVLELAPK
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LLEVVKFDVELFKASLGAGWTKPVELVVGPHTGLSYBLNERCDSSBLLELKTIAEITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQLNLSGAAKPULITLSTEELSOSLAHLLDSQYMLINANDSVEKLKGIERGETLTMEE
MQLNLSGAAKPULITLSTEELSOSLAHLLDSQYMLINANDSVEKLKGIERGETLTMEE
MQLNLSGAAKPULITLSTEELSOSLAHLLDSQYMLINGNSVYELKGIERGETLTMEE
ATTREKTPUNIDSNIELERELLTLKELIGGOFGNVYKAVYHDLEKDERIAVAVKYCK
ATTREKTPUNIDSNIELERELLTLKELIGGOFGNVYKALDEMERIAVGVCK
TDAEPADTOLILOESSLAKNEPHSNIIQLIGYCVODPMULVLELAPKGELREYLOQEK
TDAEPADTOLILOESSLAKNEPHSNIIQLIGYCVODPMULVLELAPKGELSRALDY
MULPLRILTLFCSQICDSLVYLHSTREVHRDIAARNILVCSDQCVKLADGGLSRALDY
DAVYTASRGKLEJKWLAAPESVNIRQFSMASDVWMEGVCWWEIFSLGVKPWAGVTNSDV
DAVYTASRGKLEJKWLAAPESVNIRQFSMASDVWMEGVCWWEIFSLGVKPWAGVTNSDV
TMHIEOGSRPPCPEKCPTALYNFIRSKMALEPHKRPTVDQITAIIEDDAVDCDEDEDDOD
DPGQIIVGKPWTAAGVIVAENSSLPGLTLYKTMEDQKGAEEDAKWLEGEDDEDEDDOD
IDQIPSTGHSSVENITSNGYLHTHTTSTRSLEFEDKTSRGLERSVDGVCDAVTKLQN
SFNNLTHNDDFLHSVKEVTSQLREMLIVASGMEDRYTTTORTDVMTKTLLANDMKQ
SFNNLTHNDDFLHSVKEVTSQLREMLIVASGMEDRYTTTORTDVMTKTLLANDMKQ
MSRVMGKLQVNGHQATYNTLRRDVVRICGELAVNCTTLQLQLTQPPLENEFSSLLSNC
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28818...29897,29946...30020,30070...30315,32038...32325
32760...32891)
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yk1020h08.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKASLGAGWTKPVELVVGPHTGLSYRLNERCDSSRLLELRTIAEITIRKMENGSEKTL
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/protein_id="AAM15554.1"
/db_xref="G1:20198781"
/translation="MLRITQLDHIYARHLPIGVCDEIKLEMRMREMPQSVYELQATDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="C30F8.
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/gene="C30F8.3"
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 Mismatches

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AUTHORS
TITLE
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TATTTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               TTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101;
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Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Caehorhabditis elegans clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are unknown runs of N, but the exact sizes of the gaps are unknown runs of which the exact sizes of the finished sequence this record will be updated with the finished sequence.
                                                                                                                                                               AC115614 4458 bp DNA 11hear HTG 21-MAR-2 Dictyostelium discoideum chromosome 2 map 5179259-5183715 strain
                                       Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                AC115614.1 GI:19570143
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will
                Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum
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(bases 1 to 4458)
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264136
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2053
                                                                                                                                               *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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/clone="Y119C1X"
/52713 c 52700 g 97615 t
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2052: gap of unknown length
14442: contig of 12390 bp in length
14457: gap of unknown length
101253: contig of 86796 bp in length
101268: gap of unknown length
264135: contig of 162867 bp in length
264150: gap of unknown length
299670: contig of 35520 bp in length.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                       3662 AAGATGAAGATGAAGAAGAAGATGATGAAGATGAA 3622
                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 CAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
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     AIGNER THOMAS (DE); HESS JOCHEN (DE); ROSENTHAL ANDRE (DE); RUMP ANDREAS (DE); WIRTH THOMAS (DE)
                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (Dases 1 to 49999)
                                                 Patent: WO 9950284-A 5 07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 88
                                                                                development
                                                                                  Nucleic acid molecules which code proteins influencing bone
                                                                                                                Aigner,T., Hess,J.,
                                                                                                                                                                                                                                              AX015902.1 GI:10041645
                                                                                                                                                                                                                                                                                 Sequence 5 from Patent W09950284.
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.un1-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Dictyostelium Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence and Analysis of Chromosome 2 of Dictyostelium
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Location/Qualifiers
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/chromosome="2"
/map="5179259-5183715"
complement(544. 4259)
/note="ORF_ID:dd_00748"
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535 c 4
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/strain="AX4"
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                                                                                                    Rosenthal, A., Rump, A. and Wirth, T.
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Best Local Similarity 49.88;
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Best Local Similarity
Matches 116;
                                                           9318 ATTTTGAAGAAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG 9377
                             323 CAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                         263 AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG 322
                                                                                                                                                                                                                  143 ATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG 202
                                                                                                                                                      203 ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
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                                                                                                                                                                                                                                                                                                                                                                                                          Patent: WO 9950284-A 11 07-OCT-1999;
AIGNER THOMAS (DE); HESS JOCHEN (DE); ROSENTHAL ANDRE (DE); RUMP
ANDREAS (DE); WIRTH THOMAS (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules which code proteins influencing bone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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13210 a 11814 c 10825 g 14150
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11787 c 10868 g 14209 t
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1. .49999
                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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                                                                                                                                                                                                                                                                     Score 45.8; DB Pred. No. 0.33;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA published Only in Database (2002)

2 (bases 1 to 119191)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens genomic DNA, chromosome 11 clone: CMB9-103B16, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jul 10, 2002 this sequence version replaced gi:21328197.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-FEB-2002) Masahira Hattori, The Institute of Physical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens DNA, clone: CMB9-103B16
Rump,A., Hess,J., Galgoczy,P., Wirth,T. and Rosenthal,A. Direct Submission Submitted (12-0CT-2000) Genome Analysis, Institute of Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 228283)
Rump, A., Hess, J., Galgoczy, P., Wirth, T. and Rosenthal, A.
                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                              AF312994.1 GI:18182288
                                                                                                                                                                                                                                                                                                                 Mus musculus chromosome 1 clone MML, complete sequence
                                                                                                                                                                                                                                                                                                                                       AF312994
                                                                                                                                                                                                                                   Mus musculus.
                                                                                    Unpublished
                                                                                                            Genomic sequence from mouse chr. 1
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                                                                  (bases 1 to 228283)
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/db_xref="taxon:9606"
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53.7%;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                           228283 bp
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Db 148716 ATTTTGAAGAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG 148775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 CAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG 322
                                                                                                mRNA
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                                                                                                                                                                                                                                                               mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster 1(2)01289 gene, complete cds, alternatively
                                                                                                                                                                                                                                                                                                                                                                                                  Manning,G., Micklem,D.R. and Krasnow,M.A.
Direct Submission
Submitted (16-DEC-1999) Department of Biochemistry,
University, Beckman Center, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 20796)
Manning,G., Micklem,D.R. and Krasnow,M.A.
Sequence of 1(2)01289 genomic locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF216973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
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/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                     join(<865. 1470,3154. .3310,3382. .3548,3980. .4015,
6598. .6780,6911. .7054,7117. .7250,7315. .7495,7567. .7881,
8252. .8566,8627. .9271,9325. .9507,9575. .9712,9776. .9958,
15122. .15253,15483. .15806,15871. .16059,16118. .16255,
17488. .17670,17723. .17854,18603. .18759,18817. .18983,
19047. .19203,19257. .19423,19484. .19666,19733. .20489)
                                  /product="1(2)01289 long form"
join(<1153. .1470,3154. .3310,3382. .3548,8252. .8566,
8627. .9271,9325. .9507,9575. .9712,9776. .9958,10019.
12437. .12919,13190. .14706)
/gene="1(2)01299",
                                                                                                                                                                                                                                                                                <865. .20489
/gene="1(2)0
                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
/product="i(2)01289 H9 form"
join(1257. .1470,3154. .3310,3382. .3548,3980. .4015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster
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                                                                                          .10069
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CDS

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Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                              Query Match
141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
                                                                                                                                                                                                                                                                   Local Similarity
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IDFVKTSDDDIDKEYDLPGLPALAFYRHK FRI ITGDLMKEEILEWIDLHESTADV
IESVDRKTLQVLINDVEHLAVFFYDDECESCSDILEELBIDDDTDKHGIQFVKSNDV
KLAHEIGI FAFPALVYY ETGVPIMYDGHASOODVFNHILEQKADQSIQLINRDQLFE
YIGTKDFLAVVY KEDDDDSPKVLRH ELIDDEAAEYGIY IVKHDHKLMAKKYGFRNP
PGLTVERKGKY INYDGDIDDEEEVLDWLTSPANMEMTDHIEQKADQSIQLINRDQLFE
PGLTVERKGKY INYDGDIDDEEEVLDWLTSPANMEMTDHIEQVARKMFEKIRKNSDYV
AVIFYSDECKQCPRVLAEVEHIDDEADKAGIDFVKIDDKQMAKEYGVFALPAIVFFKP
GCEQCTKVLEELENIDDDCDKHGITFVKTRDFSYADGYGVHEYPALVFFKP
GCEQCTKVLEELENIDDDCDKHGITFVKTRDFSYADGYGVHEYPALVTERGGILQNEGSVLE
LELIDDECDVFGIHWKIQDPQLAKRYSIKTFPALVYFRNGNPLLFEGGILQNEGSVLE
LELIDDECDVFGIHWKIQDPQLAKRYSIKTFPALVYFRNGNPLLFEGGILQNEGSVLE
UT TONNNBETANETERVMEDAT TOTAN BEGTT TVITERGYDNON STEETTE FEBT TETTATO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OKNDECFYVGLGHDGHSAKRGNNFVPNDYKPFQCCPTKLEKSTKVPKMTAQRIGHSEG
DQGKRPSGGNFQFASQASSKSSTKPAAIKKQAKPSKDTDDDDEDDEDKPLVKVSYANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Translation="MTFTRLKTLSLLVCALLALSFPGHVSGAGNNNNKKGSQPVAPPE PEAVIERVNAKOLEKLLADKDYVAVFWYARSCVTCDKVLAELEKIDDDTDSFGVDFVK INDKRLAKGYGIKNFPALTYFREKEPIIYDGOLMDEGGVLDFLTSLEAMDLPDRIEEV NAKILQKIIEDTDFVAVFDKDKKKAKOKILAELENIDDECOQNDTAFVKIDDKEAK EWGIDELPSIVLFERGIPHIYEGDLMKEDELLGMLVHQKRYSEIPEVTDBMKDKLVAKEDELGGTOFTANANAFREFETTHILDALI
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KILMELENIDDECEEKDIDFVKTSDDDIDKEYDLPGLPALAFYRHKFETIYTGDLMKE
EEILEWVIDLHESTADVIESVDRKTLQVLINDVEHLAVFFYDDECESCSDILEELENI
DDDTDKHGIQFVKSNDVKLAHEIGIFAFPALVYYETGVPIMYDGNLKNENRVLQWLVN
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CEPGETCEHTLNALESIDDELDEAGIIFVTTEDTGIAKKYNVKTYPRLVFFRNRDPLH
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8627. .92
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DMFGIDFVKLASIQAAKKYEIVNIPSLVYFRKQVPVLYDGDLHQHDKVITWLTSQDVF
EIKNEIEEVNRKMLDKLLEENEFLAVFFYEHNQPDSTAALEKLENIDSETDNLDITFV
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/protein_id="AAF34747.1"
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join(1257. .1470,3154. .3310,3382. .3548,8252. .8566,

join(1257. .9217.)325. .9507,9575. .9712,9776. .9958,10019. .10069,
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RILNELENIDDELEKEGIVIVRIDNAABAKEYGLDHLFALIYEENKIFALYEGDLMNE
DEVLEWILVQKKTATIEEVTDBILVTLINEHEYVVVEFTGPCEPGETCEHTLNALESI
DDELDEAGIIFVTTEDTGIAKKYNVKTYPRLVFFRNRDPLHETGDLDDEDEVLAWITD
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TMIKEGRVIAVLFYDNNDKKSQKVLEELENIDDECDALGITFYKIDNPEEAVEKGINK
VPKLIYFEKGIPTIYEGNLEDEEKLLKWLTDQTSSDQIEDITDEMLDLIIEKMPHVAV
LFYDKDQKKSQKILAELENIDDECDQNDIAFVKIDDDKEAKEWGIDEIPSIVLFERGI
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GFVK.HDEALADEYNLGNLPALVYYRHQTPIIYEGELQREEDVLEWLVQNKSTGDEDD
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8252. .8566,8627. .9271,9325. .9507,9575. .9712,9776. .9588,
15122. .15253,15483. .15806,15871. .16059,16118. .16255,
17488. .17670,17723. .17854,18603. .18759,18817. .18983,
19487. .19203,19257. .19423,19484. .19666,19733. .19920)
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/protein_id="AAF34746.1"
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Pred. No. 0.
                                                                                                                                                                           Mismatches 118; Indels
                                                                                                                                                                                                                                                  0.45;
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ACCESSION DEFINITION

AC116976

AC116976 DNA linear HTG 05-APR-20 DictyOstelium discoideum chromosome 2 map 2066573-2198571 strain AX4, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in ordered pieces.

HTG 05-APR-2002

RESULT 13

AC116976/c

BASE COUNT

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AC014497
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71008 AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 71061
                                                                                    70948 CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA 71007
                                                                                                                                                                         70888 AGAAGATAATAATAATGACGACGAAGATGACGATGAAGACGACGAGGATGACGAAGAAGA 70947
                                                                                                                                                                                                                                                                70828 TAATGATGGGGACGACGATGACGGAGATGACAATGAGGACGACGAGGACGAGGATAACGA 70887
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                                          321 TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
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                                                                                                                               261 AAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGA 320
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                                                                                                                                                                                                                    201 AGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGA 260
                                                                                                                                                                                                                                                                                                           141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
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                                                                                                                                                                                                                                                                                                                                                                                      Match 12.1%;
Local Similarity 49.6%;
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                                                                                                                                                                                                                                                                                                                                                                      116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rockville, MD, USA
This sequence was identified as CDM:10210380 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 87767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 AAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGACG 277
                                                                                                                                                                 16/062 bp DNA linear HTG 13-DEC-1999 Drosophila melanogaster chromosome 2 clone BACR10F15 (D621) RPCI-98 10.F.15 map 42E-43A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.
                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                Drosophila melanogaster.
                                                                                                         HTG; HTGS_PHASE1.
                                                                                                                              AC007624.5 GI:6563437
                                                                                                                                                       AC007624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-Koeln.de/dictyostelium/project.shtml
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Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P. Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf, Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL Submitted (21-MAY-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Dec 13, 1999 this sequence version replaced gi:5670596. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence was soon as it is available and the accession number will
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Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Perriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Gonzalez, M., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
                                                                                                                                                                                                                                                   Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 181771)
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6"
a 36877 c 36482 g 46377 t 1920 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="42E-43A"
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130045: contig of 23214 bp in length
130125: gap of unknown length
165293: contig of 35168 bp in length
165373: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165679: gap of unknown length
166287: contig of 608 bp in Length
166387: gap of unknown length
167062: contig of 695 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165293: contig of 35168 bp in length
165373: gap of unknown length
165599: contig of 226 bp in length
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49.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181771 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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Search completed: February 25, Job time: 2953 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.1%; Score 45.2; DB Best Local Similarity 49.6%; Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                      24343 AGAAGATAATAATAATGACGACGAAGATGACGATGAAGACGACGAGGATGACGAAGAAGA 24284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24403 TANTGATGGGGACGACGATGACGAGGATGACAATGAGGACGACGAGGACGAGGATAACGA 24344
                                                                                                                                                                                                                                                24283 CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA
                                                                                                                         24223 AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 24170
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                                                                                                                                                                                        321 TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGATTA 374
                                                                                                                                                                                                                                                                                                           261 AAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                     201 AGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pacleb,T., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,J.
Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
Sequencing of Drosophila chromosome 2R, region 42D-42E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA on Sep 6, 2001 this sequence version replaced gi:13374651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was assembled using end sequences from a whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="BACR07J20 (D918)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
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                                    2003, 01:54:28
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DB seq length: 2000000000
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A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
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10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries
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Compugen Ltd
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and is derived Pred. No. is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

## Score Match Length 85 13 12 11.0 111.4 111.4 111.4 111.4 111.4 111.4 111.4 111.4 111.3 111.3 110.9 110.9 110.9 110.8 110.8 ٠. 323 336 418 419 419 419 419 432 719 719 719 7148 1148 200 1038 1038 1038 DB IJ AAY94746 AAR22950 ABB69867 AAE21168 ABB66151 AAG30586 AAB29108 AAR66769 AAR98464 AAB14260 AAY50109 AAW86247 AAG58349 AAG58348 AAU76012 AAU76021 AAG33450 AAW03740 AAW95160 AAW89299 AAB19299 AAB19626 AAY78508 AAY78508 AAY68447 AAY35750 AAR44001 ABB66916 ABP27652 ABB50229 AAG58347 AAR96198 AAB14259 ABB68659 Bone morphogenetic Mouse BMP receptor Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Murine Ich-3. Mus Streptococcus poly Human transcriptio Human TRICH-12 pro Drosophila melanog Arabidopsis thalia S. cerevisiae aspa Human protein SEQ Human polypeptide Human protein SEQ rchd528 gene produ Amino acid sequenc Human rchd528 prot Human rchd528 gene Human rchd528 gene Description Zea mays protein f Arabidopsis thalia Arabidopsis thalia Mouse Ice-4 protei Murine caspase-12 Mouse Ice-4 protei Murine caspase-12 Mouse soluble BMP frugiperda immu Drosophila melanog Leech antiplatelet Platelet binding Drosophila melanog Human poly(ADP-rib Human poly(ADP-rib Amino acid sequenc Endochitinase CTS2 Amino acid sequenc Rchd528 amino acid Arabidopsis thalia Human interleukin-Mouse BMP receptor Mouse incomplete B Soluble bone morph Drosophila melanog

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## ALIGNMENTS

| PD           | PN              | SO                  | X X                              | ΚW   | KW  | XX | DE   | XX | DT                        | XX | AC        | XX | IJ                                  | RESULT 1<br>AAY94746 |
|--------------|-----------------|---------------------|----------------------------------|--|---|----|--|----|---------------------------|----|-----------|----|-------------------------------------|----------------------|
| 28-SEP-2000. | WO200056885-A1. | Hirudo medicinalis. | posterior capsule opacification. | collagen-dependent platelet adhesion inhibition; | Saratin; medicinal leech; thromboembolic disease; intraocular |    | Platelet binding inhibitor protein Saratin amino acid sequence |    | 29-JAN-2001 (first entry) |    | AAY94746; |    | AAY94746 standard; Protein; 103 AA. | LT 1<br>4746         |

Saratin; medicinal leech; thromboembolic disease; intraocular lens; collagen-dependent platelet adhesion inhibition; posterior capsule opacification.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for modifying intraocular lenses in order to lessen the thrombogenecity of the lens material, for contacting the lens surface, or for covalent crosslinking to modify the lens material. The lens material is used for refractive anterior or posterior chamber ocular implants, which may be implanted into the eye. This new type of coating avoids problems contributed by stimulated cell growth. In combination with other medicaments that are for instance conferring cell death, Saratin coating helps to completely overcome posterior capsule opacification. The antibody immunospecific for Saratin, as well as Saratin itself, are useful for measuring samples derived from host cell cultures or from a treated subject. The present sequence represents the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity: Y Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saratin is a protein isolated from the saliva of the medicinal leech Hirudo medicinalis. Saratin is an inhibitor of collagen-dependent platelet adhesion. The invention includes polynucleotide sequences encoding Saratin, an expression vector comprising the DNA sequence, a host cell transformed with the expression vector, antibodies immunospecific for Saratin, and methods for identifying Saratin agonists or antagonists. Saratin is useful for treating thromboembolic diseases, and for manufacturing a medicament for treating thromboembolic diseases. It is useful for preventing thrombotic diseases. Saratin is also useful for coating artificial surfaces, since use of Saratin renders them non-adhesive for cells and prevents the activation of cells. It may also be used for coating natural collagen surfaces. Furthermore, Saratin is useful for modifying intraocular lenses in order to lessen the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the Saratin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Saratin polypeptide and gene isolated from Hirudo medicinalis for blocking platelet adhesion, especially useful for treating or preventing thrombotic diseases, or for manufacturing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thromboembolic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAR-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERE ) MERCK PATENT GMBH
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     61
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GAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACA
                                                                                            TGCTACATCGTTTTTGAAGACACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGT
                                                                                                                                                                                                                           {\tt GluGluArgGluAspCysTrpThrPheTyrAlaAsnArgLysTyrThrAspPheAspLys}
                                                                                                                                                                                                                                                   GAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAA 123
                                                                       CysTyrIleValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGly
                                                                                                                                                  SerPheLysLysSerSerAspLeuAspGluCysLysLysThrCysPheLysThrGluTyr
                                                                                                                                                                                         TCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTAC
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99EP-0109503
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Conservative:
Mismatches:
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Gaps:
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                                   Alignment Scores:
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                                                                                                                                                   When cloned into the yeast expression vector pKH4a2, the LAPP gene sequence forms a fusion product of MAF-alpha-1 leader sequence plus mature LAPP, which when produced are proteolytically processed by the Lys-Arg cleaving endopeptidase (KEX2), which cleaves on the continuous side of Lys-Arg, and the products secreted into the culture
 Sequence
                                     conditions especially in mammals.
                                                          overcome by the addition of 0.25 \rm mM arachidonic acid. LAPP could be used for treatment and prevention of thrombotic
                                                                                   antithrombotic concentration of about 100~\text{nMolar} (or 1.6 ug/ml) Platelet aggregation is stimulated by 2 ug/ml collagen and additionable inhibits this with an IC50 of 45nM, but this may be
                                                                                                                                                                                                                                                                     New protein to inhibit collagen simulated platelet aggregation extracted from salivary gland of Haementeria officinalis for \,
                         See also AAQ23871-7.
                                                                                                                                                                                                                                  Claim 6; Page 15; 20pp; English.
                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                           LAPP blocks stimulation of platelet aggregation by collagen, at an
                                                                                                                                                                                                                                                             treating thrombotic diseases
                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ23682
                                                                                                                                                                                                                                                                                                                                                      Connolly TN,
                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAPP; collagen; platelet aggregation; antithrombotic; anticoagulant; coronary artery disease; cerebrovascular disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haementeria officinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAPP; collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leech antiplatelet protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR22950 standard; Protein; 147 AA.
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 147 AA;
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                                                                                                                                                                                                                                                                                                                                                     Keller PM
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22..147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= leader_peptide
/note= "21 hydrophobic
                                                  coronary
                                                  artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids"
                                                  cerebrovascular
                                                  disease
                                                                                                    addition
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0.172 88.50

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US-09-936-737A-1 (1-375) x AAR22950 (1-147)
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                                                                                                                                                                                                                                                                                                                                                                                                                        ABB69867
                                                                                                                                                                                                                                                                                                                                      prosophila melanogaster polypeptide SEQ ID NO 36393.
                                                                                                                                                                                                                                                                                                                                                                                       АВВ69867;
                                                                                                                                                                                                                                                                                                                                                                                                             ABB69867 standard; Protein; 368 AA.
                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ArgAsn 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 ACGGAGTAC-----TGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTAC 225
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                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 TACAAT 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                       Disclosure; SEQ ID NO 36393; 21pp + Sequence Listing; English.
                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                           N-PSDB; ABL13970.
                                                                                                         WPI; 2001-656860/75.
                                                                                                                              Venter JC,
                                                                                                                                                   (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                               interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAGTATTTCTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnLeuLeuThrLysThrGluPheThrSerValAspGluCysArgLysMetCysGluGlu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrileThrAlaGlyAsnGlyAspCysTrpSerLysArgProGlyTrpLysLeuProAsp 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrThrGlySerAspGluThrProSerThrGlyGlyGlyGlyAspGlyGlyAsnGluGlu 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleArgAlaGlnAspGluAspAlaGlyGlyAlaGlyAspGluThrSerGluGlyGluAsp 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SeralavalGluProSerCysTyrIleLeuGlnIleAsnThrGluThrAsnGluCysTyr 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
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                                                                                                                                 Li PWD,
                                                                                                                                  Myers EW;
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capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 GluPheLeuSerAlaValMetLeuLysAspTyrLysLysAla-----LeuLysTyr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 ---TTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAACATGTTTCAAGACGGAGTAC 183
                                                                                                                                                                                                           s. frugiperda immunophilin FKBP46.
                                                                                                                                                                                                                                                                             AAW68010;
                                                                                                                                                                                                                                                                                                            AAW68010 standard; Protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 CysLysLeuIleLeuClnTyrGluProAspAsnAlaThrAlaLysGluPheTyrProLeu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 TGCTACATCGTTTTTGAA------GACACGGTCAACAAGGAATGTTACTACAATGTC 234
                                                                                                                                                                                                                                               27-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 AACTTCACGGAAAAT-----------TATTTGACAGACTGCGAG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 Ile-----LeuAspLysLeuArgAlaValAlaThrSerSerAspSerAspGlu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 GTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTC-------GACGAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GCGAACAGAAATATACAGACTTCGATAAATCT-----126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 AlaSerGlyLeuProThrSerAlaSerSerGluAspLeuSerGlnSerLeuSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 GCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTAC
               Region
                                              Region
                                                                                                                             spodoptera frugiperda.
                                                                                                                                                            transplant; tissue graft.
                                                                                                                                                                            Immunophilin; moth; insect cell; nuclear; immunosuppression; drug;
                                                                                                                                                                                                                                                                                                                                                                         179 AlaAspValAspGlyAspGluAiaGlyAspAlaAspGluAspGlyAspAlaAspAlaAsp 198
                                                                                                                                                                                                                                                                                                                                                                                                        313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                           159
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                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------GluTyrThrAspAlaAspGluSerValSerAlaProThrGluPheLeuAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnTyrAsnLysSerSerSerProAspLeuAlaLeuAspLeuHisAlaSerAspValGlu 178
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24.298
12.248
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82.50
                      135..138
                                                                                               Location/Qualifiers
   /note=
                                 /note= "putative nuclear localisation signal"
                                                                  note= "EEAP motif"
 "putative nuclear localisation signal"
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                                                                                                                                                                                                           US-09-936-737A-1 (1-375) x AAW68010 (1-412)
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         163 LeuGlnLys----
                        208 GTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTT 267
                                                                         148 GACGAATGCAAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACG 207
                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the immunophilin FKBP46 from the moth Spodoptera frugiperda. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that bind to it. Such immunosuppressive agents can be used in treating
                                                                                                   136 LysalaLysProAspLysLysalaGlyLysAsnSerAlaProAlaAlaGluSerAspSer
                                                                                                                                                   116 LeuvalProAlaLysAsnLysArgLysLeuGluAsnAlaAsnAspAlaThrAlaAsnLys 135
                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                            103 AAATATACAGACTTCGATAAATCTTTTAAGAAGTCC------TCTGATCTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated immunophilin FKBP46 nucleic acids - useful for developing products for the study and identification of immunosuppressive agents for treating e.g. transplant and tissue graft patients
                                                                                                                                                                                                                                                                                                                                                               transplant and tissue graft patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX04441
                                                                                                                                                                             43 CTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTTACGCGAACAGA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alnemri ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-1996;
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                                                          AspAspAspAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-130433/11.
                                                                                                                                                                                                                                                                                                                                               412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fernandes-Alnemri T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0741134.
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292..295
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272..27
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250..256
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82.50
41.74%
27.83%
12.24%
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/note= "AP motif"
215..218
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-----PheLeuAspGlyGluAspIleAspThrAspGlu---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "putative nuclear localisation signal"
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Matches:
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Indels:
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                                                  ------GluAspGln 162
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                                            US-09-936-737A-1 (1-375) x AAR95228 (1-150)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                          Mouse soluble bone morphogenetic protein (BMP) type II receptor kinase protein-3 (BBR-3) (AAR95228) lacks the regions of the full-length receptor (AAR95224) not required for BMP binding, and is the product of a truncated cDNA sequence (AAR28023). A BMP receptor kinase protein complex formed of full-length, truncated, incomplete receptor kinase proteins (see also AAR95222-27 and AAR95229-34) is useful for screening cpds. for BMP receptor affinity or for determining the concentration of a BMP receptor ligand in a clinical with vectors carrying the appropriate DNA sequences (see also AAR95221-27).
                                                                                                                                                                                      Sequence
10 TTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA 69
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 63; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Assays for bone morphogenetic protein activities - using complex of BMP type I receptor kinase protein and BMP receptor kinase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT28024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-251887/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenbaum JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse soluble BMP receptor kinase protein-3 (BRK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9614579-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BMP type I receptor kinase; BMP receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR95228 standard; Protein; 150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 GluGluAspAspAspGluAspGluGluAspGluGluAspAspAsp 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 AATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 ---AsnAspGluSerPheLysMetAsn-----ThrSerAlaGluGlyAspAspSerAsp 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 GTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type II receptor kinase-3; BRK-3; bone morphogenetic protein;
                                                                                                                                                                                      150 AA;
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                                                                                       40.468
20.618
11.808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibroblast; cysteine box; COS; CHU; CELL CALCACC, diagnostic; bone disorder; osteogenic; drug screening; bone morphogenetic protein-agonist; reporter gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble bone morphogenetic protein receptor kinase-3 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR96200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR96200 standard; Protein; 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; bone morphogenetic protein receptor kinase-3; soluble; fibroblast; cysteine box; COS; CHO; cell culture; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1996
                                                                                                           Isolated bone morphogenic protein receptor kinase protein determine if a test cpd. is capable of binding to, or is (ant)agonist of BMP receptor kinase protein transcription
                                                                                                                                                                                                                                                                                    04-NOV-1994;
                                                                                                                                                                                                                                                                                                                    30-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                   17-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                               W09614412-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone morphogenetic protein-antagonist; hormone-responsive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTTGTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AAGAAGTCCTCTGATCTTGACGAATGCAAAAAAAACA------
The sequence represents a soluble fragment (extracellular domain) of mouse bone morphogenetic protein (BMP) receptor type-II kinase-3 (BRK-3), which induces cellular differentiation in response to BMP. A gene encoding full-length BRK-3 (AAR96198) may be isolated from
                                                                                                                                                                         N-PSDB; AAT27227
                                                                                                                                                                                                                       Nohno T, Rosenbaum JS;
                                                                                                                                                                                                                                                     (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AspLeuCysAsnValAsnPheThrGluAsnPhe 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 TTCAAGACGGAGTACTGCTACATCGTTTTTGAA------
                                                                               Claim 4; Page 60; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 GlnGlnAspLeuGlyIleGlyGluSerArgIleSerHisGluAsnGlyThrIleLeuCys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 LysGlnGlyCysTrpSerHisIleGlyAspProGlnGluCysHisTyrGluGluCysVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 AsnGlnGlu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerLysGlySerThrCysTyrGlyLeuTrpGluLysSerLysGlyAspIleAsnLeuVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GACGAAAACTTCACGGAAAATTAT 297
                                                                                                                                                                                           1996-251762/25.
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                                                                                                                                                                                                                                                                                      94US-0334179
                                                                                                                                                                                                                                                                                                                    95WO-US14085
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 116..123
                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                "Cysteine box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ArgLeuCysAlaPheLysAspProTyr 40
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 AAR95234
                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH3T3 mouse embryo fibroblast cDNA using PCR. The soluble fragment binds BMP, and has all regions not required for BMP binding deleted. Like other transforming growth factor-beta superfamily receptors, the extracellular domain of BRK-3 contains a single cysteine box. The BRK-3 receptor gene may be inserted in a vector and expressed in a CHO or COS cell culture. The receptor and antibodies against it may be used in diagnostic assays for BMP disorders, or in therapy to bind or scavenage BMPs. In addition, expression of the BRK-3 gene along with a reporter gene under the control of a hormone-responsive element in a cell culture may be used to screen compounds for BRK-agonist or -antagonist activity, by monitoring recorders agrees agrees and a cell culture may be used to screen compounds for BRK-agonist or -antagonist activity, by monitoring recorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by monitoring reporter gene expression.
                                                   Key
Domain
                                                                                                                                                    BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
                                                                                                                                                                                                                           31-DEC-1996
                                                                                                                                                                                                                                                            AAR95234;
                                                                                                                                                                                                                                                                                               AAR95234 standard;
W09614579-A1
                                                                                                      Mus sp
                                                                                                                                     BMP type I receptor kinase;
                                                                                                                                                                                        Mouse incomplete BMP receptor kinase protein-3 (BRK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 AAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACA------TGT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                               121 AspLeuCysAsnValAsnPheThrGluAsnPhe 131
                                                                                                                                                                                                                                                                                                                                                                                                     274 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ValThrThrThrProProSerIleGlnAsnGlyThrTyrArgPheCysCysCysSerThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GlnGlnAspLeuGlyIleGlyGluSerArgIleSerHisGluAsnGlyThrIleLeuCys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCTTTT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysGlnGlyCysTrpSerHisIleGlyAspProGlnGluCysHisTyrGluGluCysVal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerLysGlySerThrCysTyrGlyLeuTrpGluLysSerLysGlyAspIleAsnLeuVal 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAAGACGGAGTACTGCTACATCGTTTTTGAA----
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                                                                                                                                                                                                                                                                                                                                                                                                    -GACGAAAACTTCACGGAAAATTAT 297
                                                     Location/Qualifiers 151..172
                                    /label=
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                                                                                                                                                                                                                                                                                                 Protein;
                                      Transmembrane_domain
                                                                                                                                            BMP receptor
                                                                                                                                                                                                                                                                                                   200 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intracellular kinase domain. It is the product of a truncated cDNA sequence (AAT28030). A BMP receptor kinase protein complex formed of full-length, truncated, incomplete or soluble BRK-3 and full-length, and incomplete or soluble BRK-3 and full-length, incomplete or soluble BRK-3 and full-length, incomplete or soluble BRK-3 and full-length, and soluble BRK-3 and full-length, incomplete or soluble BRK-3 and full-length, incomplete BRK-3 and full-
                         274 -----GACGAAAACTTCACGGAAAATTAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clinical sample. The complex can be expressed by Host terms co-transfected with vectors carrying the appropriate DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse incomplete bone morphogenetic protein (BMP) type II receptor kinase protein 3 (BRK-3) (AAR95234) corresponds to the extracellular, transmembrane and intracellular juxtamembrane region of fulli-length BRK-3 (AAR95224) but is incapable of signalling due to deletion of the intracellular kinase domain. It is the product of a truncated cONA.
                                                                                           101
                                                                                                                                                                                                                                        211 AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                         169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 80; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1995;
04-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCTTTT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 TTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                 LysGlnGlyCysTrpSerHisIleGlyAspProGlnGluCysHisTyrGluGluCysVal
                                                                       ValThrThrThrProProSerIleGlnAsnGlyThrTyrArgPheCysCysCysSerThr 120
                                                                                                                                                                                                                                                                                           SerLysGlySerThrCysTyrGlyLeuTrpGluLysSerLysGlyAspIleAsnLeuVal
                                                                                                                                                                                                                                                                                                                                                     TTCAAGACGGAGTACTGCTACATCGTTTTTGAA------GACACGGTC
                                                                                                                                                                                                                                                                                                                                                                                                     GlnGlnAspLeuGlyIleGlyGluSerArgIleSerHisGluAsnGlyThrIleLeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAGTCCTCTGATCTTGACGAATGCAAAAAAAAAAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0334178
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-----ArgLeuCysAlaPheLysAspProTyr
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10 TECTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA 69

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US-09-936-737A-1 (1-375) x AAR95224 (1-1038)
                                               Query Match:
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                                                                                                                                                                    Full-length mouse bone morphogenetic protein (BMP) type II receptor kinase protein-3 (BRK-3) (AAR95224) is a receptor capable of binding BMP and transducing a signal initiated by the binding. Its amino acid sequence was deduced from a cDNA clone (AAT28020) obtd. from NIH3T3 fibroblasts. A BMP receptor kinase protein complex formed of full-length, truncated, incomplete or soluble BRK-3 and full-length, incomplete or soluble BMF type I receptor kinase proteins (see also AAR95222-23 and AAR95225-34) is useful for screening cpds. For BMP receptor affinity or for determining the concentration of a BMP receptor ligand in a clinical sample. The complex can be expressed by host cells co-transfected with vectors carrying the
                                                                                                                                           Sequence
                                                                                                                                                                appropriate DNA sequences (see also AAT28018-30).
                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 61-62; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Assays for bone morphogenetic protein activities - using complex of BMF type I receptor kinase protein and BMP receptor kinase protein
                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT28020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse BMP receptor kinase protein-3 (BRK-3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AspLeuCysAsnValAsnPheThrGluAsnPhe 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II receptor kinase-3; BRK-3; bone morphogenetic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I receptor kinase; BMP receptor
                                                                                                                                           1038 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bone morphogenetic protein type-II receptor kinase-3.
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N-PSDB; AAT27225
                                WPI; 1996-251762/25
                                                                                            Nohno T, Rosenbaum JS;
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                                                                                                                                                    (PROC ) PROCTER & GAMBLE CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTTGTT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 AsnGlnGlu----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505.
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110..112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Transmembrane region" 173..1038
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Query Match: DB: Percent Similarity: Best Local Similarity:

3.19 79.50 40.46% 20.61% 11.80%

1038 27 26 35 43

Matches: Conservative: Mismatches: Indels: Gaps: Alignment Scores:

No . :

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Isolated bone morphogenic protein receptor kinase protein - used to pT determine if a test cpd. is capable of binding to, or is (ant)agonist of BMP receptor kinase protein transcription XX Claim 1; Page 56-59; 87pp; English.

CC receptor type-II kinase-3 (BRX-3), which induces cellular differentiation in response to BMP. A gene encoding BRK-3 may be cellular domain of BRX-3 contains a single cysteine box concated near the transmembrane region. The predicted cytoplasmic cellular domain of BRX-3 contains a single cysteine box concated near the transmembrane region. The predicted cytoplasmic contein-kinase domain with predicted specificity for serine and congion contains all of the consensus sequences characterising a corpotein-kinase domain with predicted specificity for serine and congion contains, making the intracellular domain much larger than that of any other receptor in the transforming growth factor-beta congion contains against it may be used in diagnostic assays for BMP consensus sequences characterising a receptor and expressed in a CHO or COS cell culture. The receptor and antibodies against it may be used in diagnostic assays for BMP consensus sequence of a hormone-responsive element in a cell culture may be used to screen compounds for BRK-agonist or -antagonist activity, by monitoring reporter gene expression.

XX Sequence 1038 AA;
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RESULT 10
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AAW86247 standard; Protein; 1038 AA
                                                                  121 AspLeuCysAsnValAsnPheThrGluAsnPhe 131
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                                                                                                                                                                                                                                                                       {\tt SerLysGlySerThrCysTyrGlyLeuTrpGluLysSerLysGlyAspIleAsnLeuVal}
                                                                                                                                     ValThrThrThrProProSerIleGlnAsnGlyThrTyrArgPheCysCysScysSerThr 120
                                                                                                                                                                                                      {\tt LysGlnGlyCysTrpSerHisIleGlyAspProGlnGluCysHisTyrGluGluCysVal}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1038 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening method using bone morphogenetic protein receptor complex which binds to potential drugs, and ActRIIB receptor used in the complex, also host cells transfected with DNA encoding the complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 79-84; 110pp; English.
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                                                              169 TTCAAGACGGAGTACTGCTACATCGTTTTTGAA------GACACGGTC
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61 SerLysGlySerThrCysTyrGlyLeuTrpGluLysSerLysGlyAspIleAsnLeuVal 80
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DB; AAV71971.
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07-MAY-1999;
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23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                            termination sequence
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99US-0134221.
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|  |                                  |  |                         |                            |                         |   |                |                |              |                         | <u></u>        | <b>.</b>           |                | nn mi             | יוזיוזי        | ייטיטי                                 | טי טי נ                    | ַסי ָסי        | ַ פַי          | ב פ פ          | 2 12 13        | 2 2 2                   | אק<br>אק                   | PR                 | PR          | PR<br>PR  | 3                       |
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| PR 04-AUG-1999;<br>PR 04-AUG-1999;<br>PR 05-AUG-1999;<br>PR 05-AUG-1999;<br>PR 06-AUG-1999;<br>PR 06-AUG-1999; | 02-1-1                           | 27-<br>27-<br>28-                      | 23-J<br>26-J            | 22-J<br>23-J               | 22-J<br>22-J<br>22-J    | 21-J<br>21-J<br>21-J  | 20-JI          | 19-JU          | 19-JU        | 16-JU<br>19-JU          | 15-JU<br>16-JU | 13 - JU<br>14 - JU | 08-JU          | )2-JU             | )1-Jul         | 9-JUN                                  | 3 - JUN<br>4 - JUN         | 2-JUN<br>3-JUN | 1-JUN          | 8-JUN<br>8-JUN | B-JUN          | NOC-8                   | -JUN-                      | -JUN-              | JUN-        | -JUN-   | - 700                   |
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| 99; 99US-0147020; 99; 99US-0147192. 99; 99US-0147260. 99; 99US-0147361. 99; 99US-0147361.                      | 166                              | 166<br>166<br>166                      | 166<br>166<br>166       | 066<br>066<br>066          | 066<br>066<br>066       | 1066<br>1066<br>1066  | 3066<br>3066   | 3066<br>3066   | 99US         | S066<br>S066            | 99US           | 99US<br>99US       | S066           | S066              | 99US-          | -sn66                                  | 99US-                      | 9908-          | -S066          | 90s-           | 90S-(          | 90S-0                   | 908-0<br>908-0             | 90S-0              | 9US-0       | 0-sn6<br>0-sn6<br>0-sn6                         | 0-su6                   |
| US-01<br>US-01<br>US-01<br>US-01<br>US-01  | US-01<br>US-01<br>US-01          | JS-01                                  | IS-014                  | S-014<br>S-014             | S-014<br>S-014<br>S-014 | S-014<br>S-014<br>S-014   | S-014          | 5-014          | 0144<br>0144 | -0144                   | -0144          | -0143<br>-0143     | -0142<br>-0142 | 0142              | 0141           | 01409                                  | 01406                      | 01403          | 01398<br>01398 | 01394<br>01397 | 01394<br>01394 | 1394                    | )13945<br>)13945<br>)13945 | 13945              | 13945       | 13854<br>13884<br>13911                         | 13809                   |
| 47302<br>47302<br>47192<br>4726<br>4726<br>47302<br>47302  | 46388<br>46389<br>47038          | 45919<br>45919<br>45951                | 15224<br>15276<br>15913 | 5145                       | 5087                    | 5086.<br>5088.  | 4632.          | 4335.          | 1332         | 325.                    | 085.           | 542.<br>624.       | 920.           | 390.              | 154.           | 991.                                   | 323.                       | 5 U U          | 17.            | 50.            | 61.<br>62.     | 60.                     | 8 7 6                      | 5 4                | λ           | 9.70  |                         |
| 5.0.0.0.0.   | 7.7.                             |  |                         | • • •                      | •                       |   |                |                |              |                         |                |                    |                |                   |                |  |                            |                |                |                |                |                         |                            |                    |             |   |                         |
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| Alignment<br>pred. No<br>Score:<br>percent   | 28<br>29<br>29                   | 26-0CT-1<br>OR 26-0CT-1<br>OR 28-0CT-1 | 225                     | 22-                        | 21-                     | 21-1  | 14-0<br>18-0   | 14-0           | 14-0         | 13-0                    | 08-0           | 06-0               | 29-SI          | 24-SI<br>28-SI    | 22-SE<br>23-SE | 16-SE                                  | 10-SE                      | 01-SE<br>07-SE | 30-AU          | 7 - AU         | 5-AU0          | 3 - AUC                 | 0-AUG                      | 7 - AUG<br>8 - AUG | 3-AUG       | 1-AUG<br>2-AUG<br>3-AUG                         | AG                      |
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| 5.54<br>75.50<br>34.75%  | 01619                            | )1613<br>)1613<br>)1619                | 1614<br>1614<br>1613    | 16098<br>16098<br>1614     | 16081                   | 16076   | 15958          | 5963           | 5932         | 59294                   | 58232<br>58369 | 57865<br>58029     | 57117<br>57753 | 6458              | 5139           | 4039                                   | 3758                       | 2363.          | 1438.          | 1086.          | )884.<br>1065. | 930.                    | 723.                       | 426.               | 368.        | 319.  | 193.<br>935.<br>171.    |
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                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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99US-0145145. 99US-0145218. 99US-0145224. 99US-0145276.

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                                                                     AAG58347 standard; Protein;
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                                                                                                                                                                                                                                                                                     187 TACATCGTTTTTGAAGACACGGTCAACAAGGAA------ 219
                                                                                                                                                                                                                                                                                                                                   160 -----AAAACATGTTTCAAG-----ACGGAGTACTGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 PheValAsnValPhePheCysLeu-----PheLeuLeuLysThrArgserSerSerGin 54
Arabidopsis thaliana protein fragment SEQ ID NO: 75308
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| Ċ    | )139<br>)139<br>)139<br> 139                                    | )139<br>)139      | 0139         | 0139       | 0139         | 0139           | 0139 | 013              | 013          | 013          | 013   | 013          | -013             | · 013       | -013       | -013                     | -013       | -01          | -01          | -01          | 01           | 10-01     | 01           | 5-01  | 3-01       | S-01<br>S-01 | S-01         | S-01         | S-01       | S-0           | S-0                  | S-0    | -5.          | 0-Si<br>0-Si | JS-0   | 00EP-03014 |        |               | liana.       | ation ation ay;                               |            |
|      | 750.<br>763.<br>817.  | 461<br>462<br>463 | 460          | 458        | 456          | 454            | 9453 | 9452             | 8847<br>9119 | 8540         | 7724  | 7528<br>7502 | 722              | 639         | 602        | 755<br>755<br>755<br>755 | 3512       | 3476         | 3422         | 3421         | 3425<br>3421 | 3246      | 3248         | 3248  | 324        | 314          | 308          | 304          | 1300       | 1287          | 127 <b>4</b><br>1282 | 1267   | 1257         | 1231         | 1218   | 301        |        |               | •            | on;<br>gen                                    |            |
|      |   | • •               |              | • •        | • •          | •              | • •  | •                |              |              |       | .∼ .ω        |                  | ٥ <u>,</u>  |            | ο ω                      | <b>4</b> F |              | o ii         | 000          | » ö          | 33.       | . 9          |       | 07         | 8 9          | 91.          | 49.          | 45.<br>77. | 14.           | 200                  | 85.    | 88           | 180.         | 325    | 139.       |        |               |              | ; signal<br>enetic ma                         |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              |   |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | al transd<br>mapping;                         |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | transduction<br>pping; gene                   |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | ictio<br>gene                                 |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              |   |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | pathwa:                                       |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | ശേഖ   |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | р <sub>я</sub>                                |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | metabolic<br>control;                         |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | bolic<br>trol;                                |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              |   |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | pathway;<br>promoter                          |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              | ay;<br>ter;                                   |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              |   |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              |   |            |
|      |   |                   |              |            |              |                |      |                  | _            |              | _     |              |                  |             |            |                          |            |              |              |              |              |           | _            |       |            |              |              |              |            |               |                      |        |              |              |        |            |        |               |              |   |            |
|      | <b>.</b>  |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          |            |              |              |              |              |           |              |       |            |              |              |              |            |               |                      |        |              | _            |        |            |        |               |              |   |            |
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| 30   | 27 27 27  | 222               | 20           | 18<br>20   | 16<br>17     | <u> </u>       | : :: |                  | . 0          | 00           | 0 0   | 00           | 00               |             | - 0        | 0.1                      | 1 6 1      |              |              |              |              | ~ ~       | ~ ^          | ٠,    | ~ ~        | 70 ;         | æ ₹          | 70 ;         | 20 20      | <b>7</b> 0 70 | 70 !                 | ਲੇ ਲੌ  | ਲੋਂ ਨੇ       | Ď            |        |            |        |               |              |   |            |
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| -19  | G-1999;<br>G-1999;<br>G-1999;<br>G-1999;                        | 3-19              | 3-19<br>3-19 | 3-19       | 3-19<br>3-19 | G-19           | G-1: | G-1              | G-1          | ดี ดี<br>-1  | G-1   | 7-1-         | نة - 1<br>1 1    | JG-1        | ਰ-1<br>ਰ-1 | 10G-1                    | 15         | F.F.         | F :          | 4 E          | E E          | 10        | <u> </u>     | 121   | 70E-       | Jur-         | ij.          | JOT-         | ij         | Jar<br>Jar    | TOL                  | ĮĮ.    | ag d         | TOT          | įį     |            |        | ing-          | ang-<br>ang- |   |            |
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| 130  | JS-0150566<br>JS-0150884<br>JS-0151065<br>JS-0151066            | 1993<br>1990      | 1972         | 4942       | 4936         | 4856           | 4834 | 481              | 479          | 474          | 1472  | 14/3<br>1471 | 1472             | 1465 $1470$ | 1463       | 1459                     | 1459       | 145          | 145          | 145          | )145<br>)145 | )145      | 2145         | 0145  | 0144       | 0144<br>0144 | 0144         | 0144         | 0144       | 014           | 014                  | 014    | -014         | -014<br>-014 | -014   | -014       | -014   | -014          | -014         | -01   |            |
| ω.ο. | 0.4.00  | 0 N G             |              | 3 8 3      | 58           | 65.            | 41.  | 71.              | ω <u>.</u>   | 16.          | 360   | 92.          | 04.              | 389.        | 388.       | 951.                     | 919.       | 913.         | 224.<br>276. | 218.         | 192          | 680       | 580          | 980   | 1814       | 1632         | 1352         | 4334         | 4333       | 4331          | 4325                 | 4085   | 3624         | 354          | 292    | 1239       | 1215   | 1128          | 4082         | 4035  |            |
|      |   |                   |              |            |              |                |      |                  |              |              |       |              |                  |             |            |                          | •          | •            | •            |              | •            | • •       | •            | •     | •          |              |              |              | -:         | !             |                      |        |              | 2.7          | ۰.     | 00         | . 4    | 3.7 È         | - ω c        | 5.63  |            |
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                                                                                                                                                     US-09-936-737A-1 (1-375) x AAG58347 (1-336)
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13-SEP-1999;
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100 SerLeuIleSerSerAlaArgValIlePheLysIleAspSerLysTyrThrGluTyrSer 119
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                                                                                            70 CGTGAA-----GATTGTTGGACGTTTTACGCGAACAGAAATATACAGACTTCGAT 120
                                                                                                               42 PheValAsnValPhePheCysLeu-----PheLeuLeuLysThrArgSerSerSerGln 59
                                                                                                                                 10 TICTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA 69
                                                                          MetGluSerLeuLeuGluCysPheAlaIleThrAspGlyLysCysHisProAspCysLeu 79
                     -----AAAACATGTTTCAAG-----ACGGAGTACTGC 186
                                     LysAlaAsnAsnGluGlnGluAspTyrAspAlaCysGlnSerAlaAlaLeuValAlaVal 99
                                                         AAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ced-3; virally induced cell death; apoptosis; gene therapy; neural;
muscular degenerative disease; myocardial infarcation; stroke; agin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB14260 standard; Protein; 418 AA.
                                           The present sequence is a mouse Ice-4 protein sequence. The present sequence was used in a sequence homology comparison with the protein sequences of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine sequences of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14246). The coding sequence of the present sequence is a member of a family of genes involved in programmed cell death (apoptosis). Ich-1 may play an important role in both the positive and negative regulation of apoptosis. The Ich gene may be used in gene therapy in disorders characterised by cell death e.g. neural and muscular degenerative diseases, myocardial infarcation, stroke, virally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-1beta converting enzyme; ICE; cysteine protease; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Ice-4 protein sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                      New human Ich-1L and Ich-1S proteins for negative and positive regulation of programmed cell death and for developing therapeutic methods for diseases and conditions characterized by cell death, e. myocardial infarction or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1993;
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                                                                                                                                                                                                                                      Disclosure; Fig 17; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                              WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SerCysGlnTyrThrValGlyAsnLeuLeuSerTyrLeuValGluAsnValTrpThrLys 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 TACATCGTTTTTGAAGACACGGTCAACAAGGAA-----
 Sequence 418 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 TTC 285
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                                  induced cell death and aging.
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Best Local Similarity:

Percent Similarity:

7.03 75.50 54.79% 35.62%

Length:
Matches:
Conservative:
Mismatches:

Alignment Scores: Pred. No.: Score:

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DB:
This sequence represents a cDNA encoding murine caspase-12L, a splice variant of caspase-12. Caspases are a family of proteins involved in the regulation of apoptosis and are synthesised as proforms which are activated via cleavage after specific Asp residues. Mammalian cells express several caspases, and it is thought that these act in a proteolytic cascade to cause programmed cell death. Nucleic acids encoding caspase-12S (AAZ33644) or truncated forms of caspase-12L
                                                                                                                             Claim 1; Fig 1; 68pp; English.
                                                                                                                                                                   New nucleic acid encoding the short form of caspase-12, used e.g. for
                                                                                                                                                                                                                                                      Yuan J,
                                                                                                                                                                                                              N-PSDB; AAZ32645
                                                                                                                                                              treating tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caspase; splice variant; truncated; programmed cell death; apoptosis; regulation; proteolytic cascade; malignant condition; cancer; premalignant condition; solid tumour; lymphoma; chronic lymphocytic leukaemia; prostatic hypertrophy; preneoplastic liver focus; chemotherapy resistance; autoimmune disease;
                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 PheLeuGluLysThrAspMetAlaGlyLysIlePheAlaGlyHisIleAlaAsnSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 LeuLysIleGlyGluSerAlaSerPheIleLeuAsnLysAlaGluAsnLeuValGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 ValPheAspAspLeuValGluLys------AsnValLeuAsnGlyAspGluLeu 41
                                                                                                                                                                                                                         1999-620369/53.
                                                                                                                                                                                                                                                     Morishima N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAZ32646, AAZ32647) are used for production, recombinantly or in vivo, of caspase-12 polypeptides which induce programmed cell death. This is particularly useful for treating (pre)malignant conditions (e.g., solid tumours, B cell lymphoma, chronic lymphocytic leukaemia, prostatic hypertrophy, preneoplastic liver foci and resistance to chemotherapy), autoimmune diseases. The caspase-12 proteins can also be used to raise specific antibodies (for example, to determine gene expression and to screen expression libraries) or as molecular weight markers. Fragments of caspase-12-encoding nucleic acids can be used as probes to isolate the caspase-12 gene (and its allelic variants); in fluorescent in situ hybridisation for chromosomal location of the caspase-12 gene, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Northern blotting to determine caspase-12 mRNA expression in tissues
                                                                                                                                                                                                                                                                                                                                   193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                     346 GACGAG-----
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82 GluGlnLeuSerLeuGlnPheSerAsnAspGluAspAsp 94
                                                                                         62 PheLeuGluLysThrAspMetAlaGlyLysIlePheAlaGlyHisIleAlaAsnSerGln 81
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Search completed: February 25, 2003, 02:25:51 Job time : 41 secs

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US-08-044-547-3
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US-08-334-179A-8
US-09-139-600-11
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US-08-368-704C-55
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  US-09-362-230-34
pc7-US94-07926-34
US-09-134-001C-4545
US-09-134-001C-4545
US-09-254-667-1
US-08-1710-360-1
US-08-712-939B-1
US-08-961-083-200
US-08-961-083-200
US-08-961-083-200
US-09-020-684-5
US-09-020-684-5
US-09-020-683-5
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US-08-944-868A-40
US-08-944-423A-40
US-08-944-496-40
S-58502-2
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US-09-511-477-4
US-09-511-507-4
US-09-058-489-36
US-08-888-497-34
   PCT-US94-07926-41
                                                                                                                                                                                                                                                                                                                       Sequence 40, Appl
Sequence 40, Appl
Patent No. 5258502
                                                                                                                                                                                                                                                                                       Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 200, App
Sequence 6, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence
Sequence
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Sequence 5, Appli
Sequence 5, Appli
Sequence 11, Appl
Sequence 6, Appli
Sequence 13, Appl
Sequence 2, Appli
Sequence 41, Appl
Sequence 41, Appl
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Sequence 34,
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Sequence
         Sequence 41,
                                                                                                                                                                                                            36, Appl
34, Appl
34, Appl
34, Appl
34, Appl
4545, Ap
4545, Ap
1, Appli
4, Appli
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1, Appli
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## ALIGNMENTS

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; Sequence 1, Applic
; Patent No. 5324715
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                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/594,917

APPLICATION NUMBER: 1990

FILING DATE: 09-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Parr, Richard S.

REGISTRATION NUMBER: 32,586

REGISTRATION NUMBER: 32,586

REFERENCE/DOCKET NUMBER: 18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Connolly, Thomas M.
APPLICANT: Keller, Paul M.
TITLE OF INVENTION: Protein for Inhibiting
TITLE OF INVENTION: Collagen-Stimulated Platelet Aggregation
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
TELEPHONE: (908) 594-4958
TELEPHONE: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rahway
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                                                                                                                                                                                                                                                                                                                                                                                                                                  New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Merck & Co.,
P.O. Box 2000
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TELEX:

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RESULT 2
US-08-741-134-2
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Patent No. 5861498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-044-547-1
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
SOFTMARE: WordPerfect for Windows 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5861498ris
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acid
                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                119 ArgAsn 120
                                                                                                                                                                                                                                                                                                                                                                                                              226 TACAAT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 ACGGAGTAC-----TGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTAC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 SerAlaValGluProSerCysTyrTleLeuGlnIleAsnThrGluThrAsnGluCysTyr 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 AsnLeuLeuThrLysThrGluPheThrSerValAspGluCysArgLysMetCysGluGlu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 ThrIleThrAlaGlyAsnGlyAspCysTrpSerLysArgProGlyTrpLysLeuProAsp 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ThrThrGlySerAspGluThrProSerThrGlyGlyGlyGlyAspGlyGlyAsnGluGlu 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 ------CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAATATACAGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ACTACTTCTTCAGAAGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 IleArgAlaGlnAspGluAspAlaGlyGlyAlaGlyAspGluThrSerGluGlyGluAsp 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAsnSerPheLeuPheSerLeuAlaCys----SerLeuLeuValAlaTleProAla 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAAGTATTTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCA------ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: unl
                                                                                        19103
                                                                                                             Pennsylvania
                                                                                                   USA
                                                                                                                                                                                                                                      Fernandes-Alnemri, Teresa
                                                                                                                                                                                                                                                         Litwack, Gerald
Alnemri, Emad S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 amino acids
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                                                                                                                                                                                          METHODS OF USING THE SAME
                                                                                                                                                                                                                IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
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88.50
35.25%
24.59%
13.13%
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Sequence 3, Application US/08044547

Patent No. 5324715

GENERAL INFORMATION:
APPLICANT: Connolly, Thomas M.
APPLICANT: Keller, Paul M.
TITLE OF INVENTION: Collagen-Stimulated Platelet Aggregation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INCORPATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
                                                                                       CORRESPONDENCE ADDRESS:
COUNTRY: UZIP: 07065
                                          STREET: P.O. CITY: Rahway
                                                                                                                                                                                                                                                                              194 GluGluAspAspAspGluAspGluGluAspGluGluAspAspAsp 208
                         STATE: New Jersey
                                                                     ADDRESSEE: Merck & Co., Inc.
                                                                                                                                                                                                                                                                                                              328 AATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                                                                                                                                                                                                           177 ---AsnAspGluSerPheLysMetAsn-----ThrSerAlaGluGlyAspAspSerAsp 193
                                                                                                                                                                                                                                                                                                                                                                         268 GTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGT 327
                                                                                                                                                                                                                                                                                                                                                                                                           163 LeuGlnLys-------PheLeuAspGlyGluAspIleAspThrAspGlu--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                        208 GTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 Aspaspaspasp------GluaspGln 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GACGAATGCAAAAAAAACATGTTTCAAGACGGAGTACTGCTACATGGTTTTTGAAGACACG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 LysalaLysProAspLysLysalaGlyLysAsnSerAlaProAlaAlaGluSerAspSer 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AAATATACAGACTTCGATAAATCTTTTAAGAAGTCC------TCTGATCTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 LeuValProAlaLysAsnLysArgLysLeuGluAsnAlaAsnAspAlaThrAlaAsnLys 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 CTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGAACGTTTTTACGCGAACAGA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/741,134 PILING DATE: CLASSIFICATION: 424
                                                           P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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27.838
12.248
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Matches:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/594,917
FILING DATE: 09-007-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
..
                                                                                                                                                                                                                                APPLICANT: ROSENBAUM, JAN S.
APPLICANT: NOHNO, TSUTOMU
TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parr, Richard S. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
CURRENT APPLICATION DATA:
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAAT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 TCCTCTGATCTTGACGAATGCAAAAAAAAACATGTTTCAAGACGGAGTAC-----TGC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908) 594-4720
TELEX: 138825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 AspCysTrpSerLysArgProGlyTrpLysLeuProAspAsnLeuLeuThrLysThrGlu 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCTTTTAAGAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                               85 TyrileLeuGlnIleAsnThrGluThrAsnGluCysTyrArgAsn 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 PheThrSerValAspGluCysArgLysMetCysGluGluSerAlaValGluProSerCys 84
                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
                                                                                                            ZIP: 45061
                                                                                                                                                                       ADDRESSEE: 'THE TWO-LESSEET: 11810 EAST MIAMI RIVER ROAD
                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                               US
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80.50
50.91%
32.73%
11.94%
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US-09-936-737A-1 (1-375) x US-08-334-179A-10 (1-150)
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Best Local Similarity:
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                                                                                                                                                                                                            Sequence 8, Application US/08334179A; Patent No. 6306622
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                                                                                                                                GENERAL INFORMATION:

APPLICANT: NCHNO, TSUTOMU

APPLICANT: NCHNO, TSUTOMU

TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 54 TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                               121 AspLeuCysAsnValAsnPheThrGluAsnPhe 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SerLysGlySerThrCysTyrGlyLeuTrpGluLysSerLysGlyAspIleAsnLeuVal 80
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                                 COUNTRY:
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                                                                                    11810 EAST MIAMI RIVER ROAD
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Matches:
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Indels:
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US-09-187-789-16
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                                                                                                                                                    Sequence 16, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
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Best Local Similarity:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-334-179A-8
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
                                                                                                                                                                                                                                                                   121 AspLeuCysAsnValAsnPheThrGluAsnPhe 131
                                                                                                                                                                                                                                                                                                                                    101 ValThrThrPtoProSerIleGlnAsnGlyThrTyrArgPheCysCysCysSerThr 120
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NAME: CORSTANJE, BRAHM J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 GlnGlnAspLeuGlyIleGlyGluSerArgIleSerHisGluAsnGlyThrIleLeuCys 60
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REFERENCE/DOCKET NUMBER: 5473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/334,179A FILING DATE: 04-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
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GY: linear
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N: 435
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                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-09-139-600-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 11
LENGTH: 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alnemri, Emad S.
APPLICANT: Pernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHOD OF USE
FILE REFERENCE: 480140.434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/139,600 CURRENT FILING DATE: 1998-08-25 NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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295 TATTTG-----ACAGACTGCGAGGGTAAA---GATGCAGGTAATGCGGCAGGTACAGGT 345
                                                                                                                                             193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                     253 -----GACCAAGAAAATTTGTTGTCGAC-----GAAAACTTCACGGAAAAT 294
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                                    42 LeuLysIleGlyGluSerAlaSerPheIleLeuAsnLysAlaGluAsnLeuValGluAsn 61
                                                                                                            26 ValPheAspAspLeuValGluLys-----AsnValLeuAsnGlyAspGluLeu 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 ValPheAspAspLeuValGluLys------AsnValLeuAsnGlyAspGluLeu 41
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75.50
54.798
35.628
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                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-258-287B-58
                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application US/082582878 Patent No. 6083735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                              193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
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                                         295 TATTTG-----ACAGACTGCGAGGGTAAA---GATGCAGGTAATGCGGCAGGTACAGGT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/258,287B FILING DATE: 10-JUN-1994
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62 PheLeuGluLysThrAspMetAlaGlyLysIlePheAlaGlyHisIleAlaAsnSerGln 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bugaisky, Lawrence B REGISTRATION NUMBER: 35,08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
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                                                                                   42 LeuLysIleGlyGluSerAlaSerPheIleLeuAsnLysAlaGluAsnLeuValGluAsn 61
                                                                                                                                                                       26 ValPheAspAspLeuValGluLys------AsnValLeuAsnGlyAspGluLeu 41
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RESULT 9
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 10-JUN-1S
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/0
FILING DATE: 24-UUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B
REGISTRATION NUMBER: 35,08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 4-JAN-1995
CLASSIFICATION: 435
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   295 TATTTG-----ACAGACTGCGAGGGTAAA---GATGCAGGTAATGCGGCAGGTACAGGT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 248636 SSK
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                                  42 LeuLysIleGlyGluSerAlaSerPheIleLeuAsnLysAlaGluAsnLeuValGluAsn
                                                                                                            26 ValPheAspAspLeuValGluLys------AsnValLeuAsnGlyAspGluLeu 41
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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amino acid
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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Patent No. 6083735
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 06.09.3920001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100.371-2600
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                            193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                        295 TATTTG-----ACAGACTGCGAGGGTAAA---GATGCAGGTAATGCGGCAGGTACAGGT 345
                                                                                                      253 ------GACCAAGAAAATTTGTTGTCGAC-----GAAAACTTCACGGAAAAT 294
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62 PheLeuGluLysThrAspMetAlaGlyLysIlePheAlaGlyHisIleAlaAsnSerGln 81
                                                                              42 LeuLysIleGlyGluSerAlaSerPheIleLeuAsnLysAlaGluAsnLeuValGluAsn 61
                                                                                                                                                            26 ValPheAspAspLeuValGluLys-----
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Matches:
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Indels:
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| 22    | 3 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA   | VQ YG   |
|       | 09-936-  | us-   |
|       | Alignment Scores:  Pred. No.:  0.64  Score:  75.50  Matches:  26  Percent Similarity:  54.798  Best Local Similarity:  35.628  Query Match:  11.208  DB:  Alignment Supplies:  74.798  Matches:  14  Mismatches:  14  Gaps:  6 | Ali<br>pre<br>Sco<br>Per<br>Bes<br>Que<br>DB: |
|       | TYPE:<br>TOPOLOG<br>MOLECULE<br>-08-368-704C   | us-;  |
|       | LENGTH: 419 amino acids  | ·· ·· ··                                      |
|       | TELEFAX: (202) 371-2540<br>TELEX: 248636 SSK   |   |
|       | TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600  | · · · · ·                                     |
|       | ATTORNEY/AGENT INFORMATION:  NAME: Buggisky, Lawrence B.  REGISTERATION MITTHER 125 086  |   |
|       | APPLICATION NUMBER: US 08/080,850 FILING DATE: 24-JUN-1993   |   |
|       | CLASSIFICATION: 435 PRIOR APPLICATION DATA:  | ٠. ٠.   |
|       | APPLICATION DATA:  APPLICATION UMBER: US 08/258,287  FILING DATE: 10-JUN-1994  |   |
|       | FILING DATE: 4-JAN-1995 CLASSIFICATION: 435 DBIOD NOTICE 435   |   |
|       | CURRENT APPLICATION NUMBER: US/08/368,704C   | ٠. ٠.   |
|       | OPERATING SYSTEM: PC-DOS/MS-DOS<br>SOFTWARE: Patentin Release #1.0, Version #1.25  |   |
|       | MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible   | ٠. ٠.   |
|       | ZIP: 20005<br>COMPUTER READABLE FORM:  | ٠. ٠.   |
|       | STATE: D.C. COUNTRY: USA   | ٠. ٠.   |
|       | Suite 600  | ٠. ٠.   |
|       | oldstein   | ٠. ٠.   |
|       | NUMBER OF SEQUENCES: 95  | ٠. ٠.   |
|       | ANT: Yuan, Junying<br>ANT: Miura, Masayuki   |   |
|       | INFORMATION:   |   |
|       | SULT 1<br>-08-36<br>Sequen   | US<br>;                                       |
|       | 82 GluGlnLeuSerLeuGlnPheSerAsnAspGluAspAsp 94  | DЬ  |
|       | 346 GACGAGTCAGATGAAGTTG  | Qγ  |

RESULT 12 US-08-616-844-40

346 GACGAG---

82 GluGlnLeuSerLeuGlnPheSerAsnAspGluAspAsp 94

---TCAGATGAAGTTGAT 366

Sequence 40, Application US/08616844 Patent No. 5849578

NERAL INFORMATION: APPLICANT: FALB, DEAN A.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE NUMBER OF SEQUENCES: 54

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

STREET:

New York New York

ADDRESSEE:

E: PENNIE & EDMONDS 1155 Avenue of the Americas

COUNTRY: STATE:

USA

10036-2711

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| US-08-59-64-40  US-08-59-64-40  Sequence 40, Application US/0859964  Patent No. 5882925  Patent No. 5882925  PATENTE OF INVENTION: COMPOSITIONS AND METHODS FOR THE ITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE INDRESSERS: PENNIE & EDMONDS  STREET: 1.155 AVENUE & EDMONDS  CORRESSORE PENNIE & EDMONDS  STREET: 1.155 AVENUE & EDMONDS  COMPUTER: New York  COUNTRY: New York  COUNTRY: New York  COMPUTER REDARLE FORM:  APDICATION ATTELL OF TAXABLE FORM:  APPLICATION MUMBER: US/08/59,654  FILING DATE: 09-FEB-1996  CLASSIFICATION NUMBER: US/08/59,654  PELING DATE: 09-FEB-1996  PRIOR APPLICATION NUMBER: US/08/59,654  PRIOR APPLICATION NUMBER: US/08/386,444  PRICESTRATION UNMBER: |  |

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/599.654

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

O9-FEB-1996

PRIOR APPLICATION NUMBER: US 08/485.573

PRIOR APPLICATION NUMBER: US 08/386.844

PRIOR APPLICATION NUMBER: US 08/386.844

PLICATION NUMBER: 10-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: CORUZZI, LAURA A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-053

REFERENCE/DOCKET NUMBER: 790-9090

TELEFAN: (212) 790-9090

TELEFAN: (212) 790-9090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM CC compatible

COMPUTER: ISM CC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/616,844

FILING DATE: 15-MAR-1996

FILING DATE: 15-MAR-1996

CLASSIFICATION:

US-08-616-844-40

MOLECULE TYPE: protein

TOPOLOGY: STRANDEDNESS:

unknown

TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids

amino acid

Alignment Scores:

Pred

No.:

Length: Matches:

Percent Similarity:

Best Local Similarity:

39.04% 29.45% 11.37% 1.44

Gaps: Mismatches: Conservative: Indels:

Query Match:

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784 SerHisHisLeuPheSerSerIleLeuProSerThrArgAlaSerValHisLeuLeuLys 803  US-09-936-737A-1 (1-375) x US-08-616-844-40 (1-1481)

764 SerSerSerSerSerSerSerSerGlyProProLeuProLeuProSerValSerGln 783

Alignment Scores:

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US-08-944-868A-40

// Sequence 40, Application US/08944868A

Patent No. 6018025
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                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: FALE, DEAN A

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 10-FEB-1995
                                                                              PRIOR APPLICATION DATA:
                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     STREET: LICATORY: New York
                                                     APPLICATION NUMBER: FILING DATE:
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                                                                                                 CLASSIFICATION:
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Patent No. 6020463
GENERAL INFORMATION:
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Best Local Similarity:
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                     CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                           APPLICANT: FALE, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
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NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                889 ValileThrGluSerLys 894
     STATE:
                                                                                                                                                                                                                                                                                                                                       116 AAGTCTGTATATTTTCTGTTCGCGTAAAACGTCCAACAATCTTCACGTTCTTCTGAAGAA 57
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New York
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APPLICATION NUMBER: US 08/599,654

FILING DATE: 09-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,573

FILING DATE: JUN-07-1995

PRIOR APPLICATION NUMBER: US 08/386,844

APPLICATION NUMBER: US 08/386,844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
116 AAGTCTGTATATTTTCTGTTCGCGTAAAACGTCCAACAATCTTCACGTTCTTCTGAAGAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
                                     864 ThrSerPheMetThrMetLeuHisSerSerGlnThrAlaAsp---LeuLys----- 879
                                                                        164 ------GTTTTTTGCATTCGTCAAGATCAGAGGACTTCTTAAAAGATTTATCG 117
                                                                                                             844 ThrProValLeuProArgAlaArgGluThrProValThrSerPheGlnThrSerThrMet 863
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                         323 ------GCATCTTTACCCTCGCAGTCTGTCAAATAATTTTCCGTGAAG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 TCTTCATCAACTTCATCTGACTCGTCACCTGTACCTGCCGCATTACCT----- 324
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Conservative:
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Db 880 -----SerGlnSerThrProHisGlnGluLys 888

Qy 56 GTAGTTGAGATCAGCAAG 39

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Db 889 ValileThrGluSerLys 894

Search completed: February 25, 2003, 02:29:51 Job time: 17 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-DB=-Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-biosun62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09936737_CCCN_11_2_@TUNAT_14022003_100558_1452
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MAMP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL-frame+_n2p.model -DEV-x1h
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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Sequence 16, Appl
Sequence 9, Appli
Sequence 40, Appl
Sequence 60, Appl
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| Sequence 8, Appli                       | 0 US-09-946-805-8  |            |            | 9.4  | ω           | <b>4</b> 5   |
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| equence 1031, A                         | US-09-925-301-10   |            |            | •    |             | 44           |
| equence 206                             | US-09-801-368-206  |            | _          |      | w<br>·      | 43           |
| 52, 1                                   | US-10-042-417-52   |            | -          | •    | 64          | 42           |
| equence 7, Appl                         | US-09-416-384A-    |            | •          | •    |             | 41           |
| ce 16                                   | US-09-745-763-1    |            | •          | •    | 64          | 40           |
| 25, Ap                                  | US-10-125-852-2    |            | •          | •    |             | 39           |
| equence 23, App                         | US-10-125-852-2    |            | •          |      | 64          | 38           |
| e 4, Appl                               | US-10-185-770-4    |            | _          | •    | _           | 37           |
| e 2,                                    | -806-60-SD         |            |            |      | 4           | 36           |
| equence 2, Appl                         | US-09-973-451-2    |            |            | •    |             | ω<br>G       |
| e 511                                   | US-09-925          |            |            |      | 4           | ω (          |
| quence 2,                               | US-09-759-508B-2   | 5926 9     | ν.         | 9.6  | ص<br>د<br>د | ω c          |
| sequence 1                              | 115-00-815-242-1   |            |            | •    | n C         | ) L          |
| 114. App                                | TS-09-974-         |            |            | D. 0 | no          | 3 2          |
| o a                                     | 05-09-820          |            |            |      | י ט         | 2 2          |
| ednembe c                               | 028-00-31          |            |            | •    | י ס         | ) (C         |
| equence 4, Appl                         | 028-60-50          |            |            | •    | 0           | 27           |
| equence 2, Appi                         | US-09-820-         |            |            | 9.6  | 65          | 26           |
| equence 3                               | US-09-816-         |            |            | •    | 5           | 25           |
| 11                                      | US-09-808-602-110  |            | N          | 9.7  | 65.5        | 24           |
| equence 11                              | US-10-140-3        |            |            | •    | 66          | 23           |
| 6                                       | us-10-085-         |            |            | •    | 66          | 22           |
| ī, Appli                                | US-10-087-1        |            |            | •    | σ.          | 21           |
| Sequence 57, Appl                       | US-09-801-57       |            |            | 9.9  | 66.5        | 20           |
| ce 3, Appl                              | US-09-872-52       |            |            |      | σ.          | 19           |
| equence 18                              | US-10-135-322·     |            | _          |      |             | 18           |
| equence 4,                              | US-09-918-508-4    |            | 10         |      | 7           | 17           |
| quence 28:                              | US-09-895-913A     |            | N          |      | 7           | 16           |
| equence 4:                              | US-09-801-368-42   |            | υı         |      | 68          | 5            |
| equence 7                               | US-09-993-999-7    |            | <b>—</b> . |      | n :         | 14           |
| quence 65:                              | US-09-738-626-653  |            | 2          | 10.2 | 58.5        | ا ب<br>ا     |
| equence 5:                              | US-09-764-860-55   | N I        |            |      | י סכ        | ٠<br>ا بـ    |
| equence 200, Ap                         | US-09-765-272-200  | . 4        | ٥ <u>ا</u> |      | Φ,          | 1 5          |
| equence 1                               | US-09-815-242-11   | 7          | 1 ,        |      | ٠,          | 5            |
| e 2, Appl                               | US-09-821-839-2    | ω (        | UI !       |      |             | ه م          |
| equence 252                             | US-09-833-790-252  | א עכ       | <u> </u>   |      | 71 5        | <b>x</b> 0 ~ |
| equence 2038, A                         | US-09-867-550-20   | <i>u</i> c | _ (        | •    | ۱.          | <b>1</b> C   |
| Sequence 62, Appli                      | ) US-09-801-368-82 | 10 75      | 56<br>07   | 10.9 | 73.5        | n Ω          |
| 200000000000000000000000000000000000000 | 110 00 001 160 0   | ,          | 1          |      | ,           |              |

## ALIGNMENTS

RESULT 1 US-09-989-903-16

Sequence 16, Application US/09989903 Patent No. US20020146804A1

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Percent Similarity:
Best Local Similarity:
                                                                                                                                              ; ORGANISM: Mus musculus US-09-989-903-16
                                                                                                                                                                                                                                                                                                                              ; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: FERNANDEZ-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434D1
  Query Match:
                                                                Score
                                                                                                     Alignment Scores:
                                                                                   Pred. No.:
                                                                                                                                                                                                                               SEQ ID NO 16
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/989,903
CURRENT FILLING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                      TYPE: PRT
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0.84
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54.79%
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11.20%
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; Sequence 40, Application US/09371900
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                      US-09-371-900-40
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US-10-041-856-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-0
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PATENTIN VER: 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: SLAUGENHAUPT, SUSAN
APPLICANT: GUSELLA, JAMES F.
TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
TITLE OF INVENTION: DYSAUTONOMIA
FILE REFERENCE: 1829-4004US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10041856 Patent No. US20020169299A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/041,856
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 60/260,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1178
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                                                                                                                                                                                                                          440 TyrSerAsnProPhePheArgLysLysTyrIleLeuGluIleLeuLysValProSerHis 459
                                                                                                                   229
                                                                                                                                                     460 LysThrTyrPheAlaCysPheAlaValSerGlnAspThr-----
                                                                                                                                                                                        172 AAGACGGAGTAC---TGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTAC 228
                                                                                                                                                                                                                                                                 420 IleThrSerAspTrpLysIleIleSerCysMetLeuPhePheLysLysLysLysArgAsn 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 ------GACCAAGAAAATTTGTTGTCGAC-----GAAAACTTCACGGAAAAT 294
                                                                                                                                                                                                                                                                                                                                                                                                        19 TCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 TATTTG-----ACAGACTGCGAGGGTAAA---GATGCAGGTAATGCGGCAGGTACAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GluGlnLeuSerLeuGlnPheSerAsnAspGluAspAsp 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PheLeuGluLysThrAspMetAlaGlyLysIlePheAlaGlyHisIleAlaAsnSerGln 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 LeuLysIleGlyGluSerAlaSerPheIleLeuAsnLysAlaGluAsnLeuValGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 ValPheAspAspLeuValGluLys-----AsnValLeuAsnGlyAspGluLeu
                                                                                                               AATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAA
                                                                                                                                                                                                                                                                                                                                              -----GATTGTTGGACGTTTTACGCGAACAGAAAATATACA 111
                                                                                                                                                                                                                                                                                                                                                                                    SerIleGlnCysLeuSerAspIleValAlaTyrThrThrSerThrHisHisValHisVal 419
                                                                      -AspGlyTyrLysPheAsnSerAspArgAlaSerIleAspGlu 486
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GENERAL INFORMATION:
APPLICANT: FALE, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
824 ThrThrSerThrSerAlaProLeuSerValSerGlnThrThrLeuProGlnSerSerSer
                     233 ACATTGTAGTAACATTCCTTGTTGATGCACCGTGTCTCAAAAACGATGTAGGAGGTACTCC--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                764 SerSerSerSerSerSerSerSerGlyProProLeuProLeuProSerValSerGln 783
                                                                                                                                                                                                                                                                                          371 TCTTCATCAACTTCATCTGACTCGTCACCTGTACCTGCCGCATTACCT------
                                                                                                                                                                 784 SerHisHisLeuPheSerSerIleLeuProSerThrArgAlaSerValHisLeuLeuLys 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
TELEX: 66141 PENNIE
                                                                                SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                        TTTTCGTCGACAACAATTTTTCTTGGTCTAACTCT---TCACCA-----TCAACG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/371,900 FILING DATE: 11-Aug-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CORUZZI, LAURA A REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1481 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                         -----GCATCTTTACCCTCGCAGTCTGTCAAATAATTTTCCGTGAAG 282
                                                                                                                                                                                                                                                                                                                                                                                                   39.04%
29.45%
11.37%
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74.00
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US-09-924-417-60

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164 ------GTTTTTTGCATTGGTCAAGATCAGAGGACTTCTTAAAAGATTTATCG 117

116 AAGTCTGTATATTTTCTGTTCGCGTAAAACGTCCAACAATCTTCACGTTCTTCTGAAGAA 57

176 -----GTCTTGAAACAT

844 ThrProValleuProArgAlaArgGluThrProValThrSerPheGlnThrSerThrMet 863

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RESULT 4 US-09-924-417-60

; sequence 60. Application US/09924417 patent No. US20020142441A1 GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE NUMBER OF SEQUENCES: 67

NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas

SETWARE: FASTSEO VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/924,417
FILING DATE: 07-Aug-2001

PRIOR APPLICATION DATA:

CLASSIFICATION: <Unknown>

IOR APPLICATION UMER: US/09/034,286
FILLING DATE: 04-MAR-1998
FILLING DATE: 04-MAR-1998
FILLING DATE: 06-JUN-1997
FILLING DATE: 06-JUN-1997
APPLICATION NUMBER: 08/799,910
APPLICATION NUMBER: 08/799,910
FILLING DATE: 13-FEB-1996
FILLING DATE: 16-FEB-1996
APPLICATION NUMBER: 08/599,654
APPLICATION NUMBER: 08/599,654
FILLING DATE: 09-FEB-196
FILLING DATE: 09-FEB-196
FILLING DATE: 09-FEB-196
FILLING DATE: 07-FEB-196
APPLICATION NUMBER: 08/386,844
FILLING DATE: 10-FEB-195

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COUNTRY CITY: New York

USA

COMPUTER: IBM Compatil OPERATING SYSTEM: DOS

IBM Compatible

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889 ValileThrGluSerLys 894

GTAGTTGAGATCAGCAAG 39

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids

TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TYPE: amino acid STRANDEDNESS: single

NAME: COTUZZI, LAUTA A, 742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-114-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7999090
TELEPAX: (212)8699741
TELEFAX: (212)8699741

ATTORNEY/AGENT INFORMATION

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Query Match:
                        Best Local Similarity:
                                                                                       Alignment Scores:
                                           Percent Similarity:
                                                                                                                           US-09-973-451-4
                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 976
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                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE
TITLE OF INVENTION: (PARG) ENZYMES,
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE OF INVENTION: THEREWITH
FILL REFERENCE: NIAD 201
CURRENT FILING DATE: US/09/973,451
CURRENT FILING DATE: 2001-10-09
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                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/09/302,812
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,768
PRIOR FILING DATE: 1998-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09973451 patent No. US20020132328A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 38
                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JACOBSON, Myron K. APPLICANT: JACOBSON, Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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Best Local Similarity:
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: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-801-368-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                          No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 ThrLeuSerSerGlnIleThrSer 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 ATGCGGCAGGTACAGGTGACGAGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 LeuGlyThrThrThrThrGluSerThrLeuAsnSerValAlaIleThrSerMetLysThr 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 TTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 IleThrGlnThrThrLysThrLeuThrSerSerThrLysThr-----LysSerSer 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 TCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 ThrGlnSerLysSerLysValThrLeuSerProThrAlaSerSerAlaIleLysThrSer 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 ACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 SerAlaSerThrSerSerAlaSerThrSerGlnLysLysThrThrGlnSerThrThrSer 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AlaSerGlnThrAlaThrThrThrValAlaThrSerLysThrSerAlaAlaSerThrSer 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 GCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGT 88
                                                                                                                                                                                                                                                                                                                                                                                                                     JACOBSON, Elaine L.
AM, Jean-Christophe
                                                                                                                                                                                                                                                                                                                                                                                                              LIN, Winston
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72.50
38.89%
25.93%
10.76%
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73.50
39.81%
25.00%
Indels:
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                                               Matches:
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Matches:
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CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 143
                                                                                                                                                                            US-09-936-737A-1 (1-375) x US-09-867-550-2038 (1-143)
                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                US-09-867-550-2038
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TITLE OF INVENTION: NO. US20020082206Alel Polynucleotides from Atherogenic Cells a
TITLE OF INVENTION: Thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-936-737A-1 (1-375) x US-09-973-451-4 (1-976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Leach, Martin D. APPLICANT: Mehraban, Fuad, APPLICANT: Conley, Pamela
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
130 AAGAAGTCCTCTGATCTTGACGAATGCAAAAAAAACATGTTTCAAGACGGAGTACTGCTAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                34 -----CysLeuHisThrPheCysLys-----ThrCysTleValGlnHisPhe 47
                                                                 70 CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCTTTT 129
                                                                                                  15 TyrrleThrCysTyrrleCysLysGlyTyrLeurleLysProThrThrValThrClu--- 33
                                                                                                                                  10 TPCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 ValGlyThrGlySerLysAsnAsp 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 GCAGGTACAGGTGACGAGTCAGAT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 GACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 AlaSerCysGlnGlnAspGluIleAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 AAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 TGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTCAAC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AlaAsnAlaLysGlnThrThrGluAspGluHisAlaArgGluAlaLysSerHisGlnLys 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 SeraspThraspSerGluGluasnArgAspAsnGlnglnpheLeuThrThrValLysLeu 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 GCGAACAGAAATATACAGACTTCGATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 TCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTT-----TAC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mehraban, Fuad,
Conley, Pamela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 252
LENGTH: 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 TTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGAT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 MetLeuArgLeuAspAsnThrLeuGluGluIleIlePheLysLeuValProGlyLeuArg 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48
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313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                        107 AspAspArg-----IleIleArgThrAspTrpAspAlaGlyPheLys------Glu 121
                                                                                    253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
                                                                                                                                                                     193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCAGAAGAACGTGAA------GATTGTTGGACGTTTTACGCGAACAGAAAA 105
                                                                                                                                                                                                                                                                                                  49 PheTyrThrThrGluGluGlnIleTyrGluLeuPheSerLysSerGlyAspIleLysLys 68
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29 AsnGluGluGlnGluLysLeuLeuLysLysSerCysThrLeuTyrValGlyAsnLeuSer 48
                                                                                                                                                                                                              69 IleIleMetGlyLeuAspLysMetLysLysThrAla-----CysGlyPheCysPheVal 86
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                                                                                                                                                                                                                                                         ------CTTGACGAATGCAAAAAAAACATGTTTCAAGACGGAGTACTGCTACATC 192
                                                                                                                            GluTyrTyrSerArgAlaAspAlaGluAsnAlaMetArgTyrIleAsnGlyThrArgLeu 106
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Indirias, Carol Y.
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US-09-821-839-2
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                                                                                                                                                                                                                                                                   RESULT 10
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APPLICANT: Ma, Hong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/821,839
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,523
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Plant Gene Required for Male Meiosis FILE REFERENCE: Psu-0020
                                                                                                                                                                                                              Sequence 11522, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 7
                                                                                      APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                          APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                    APPLICANT:
                                                                                                                                            APPLICANT:
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No.:
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                                                                                                                                                                                                                                                                                                                                                                        345 AspAspGluGluValGluGluSerTyrLeuArgLeuArgGluArgGluArgSerHisAla 364
                                                                                                                                                                                                                                                                                                                                                                                                          238 GATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAAT--- 294
                                                                                                                                                                                                                                                                                                                                                                                                                                            325 IleProAsnAspPheGlySerSerCysGluGluGluIleHisSerGluLeuLeuArgPhe 344
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                                                                                      Trawick, John D. Carr, Grant J.
                                                                                                                                           Zyskind, Judith W.
                                                                                                                             Wall, Daniel
                                                          Xu, H. Howard
                                                                     Yamamoto, Robert T.
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70.50
37.61%
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                                           of Essential Genes in
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US-09-765-272-200
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                                                                                                                                                                                                                                                                                                                                                              Sequence 200, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 TTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 ProThrLys------LeuGlyAspArgAsnTyrTrpGluAsnPhe 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
FILING DATE: 22-Jan-2001
           APPLICATION NUMBER: US/09/765,272
                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                          STATE: Maryland
                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                        20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---IleLeuLeuGlnAspLeuAlaAsn-----AlaValTyrAsnValMet 273
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; ORGANISM: Homo sapiens US-09-764-860-558
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Best Local Similarity:
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                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 558
LENGTH: 72
TYPE: PRT
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                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       Sequence 558, Application US/09764860 Patent No. US20020094953A1
                                                                                                     Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/764,860 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                          FILE REFERENCE: PC008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 200: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       389 LeuPheAlaThrAspLeuGlnAspTyrProLeuAlaAlaValArgAspPheGlyGlyArg 408
                                                                                                                                                                                                                                                                                                                                                                       409 AlaTyrPheGlyGlnGlu 414
                                                                                                                                                                                                                                                                                                                                                                                                            334 GCAGGTACAGGTGACGAG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 GAGTTAGACCAAGAAAATTT-------GTTGTCGACGAAAACTTCACGGAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 GluIleIleAsnCysArgValThrSerGluGlnIleSerCysTyrLysSerAspIleSer 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 200:
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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// ORGANISM: Corynebacterium glutamicum
US-09-738-626-6537

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Best Local Similarity:
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MNDO, SEIKO
APPLICANT: HAVASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6537
LENGTH: 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                            134 AGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCG 193
149 AspLeuProThrArgGlu---ArgAspValLeuThrLeuLeuHisLeuGlyLysSer---
                                   194 TTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAG 253
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Matches:
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RESULT 15
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                   APPLICANT:
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                                                                                                                                                                      Sequence 426, application US/09801368 Patent No. US20020128250A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
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                                                                                                                                APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Arm, Jonathan P.
APPLICANT: Austen, K. Frank
APPLICANT: Glimcher, Laurie H.
TITLE OF INVENTION: Phospholipase A2 Group Preferentially
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REFERENCE: HUI-046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/246,316
PRIOR FILING DATE: 2000-11-06
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   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 146
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                        262 AAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGAT 321
                                                                                                                                                                                                                                                                                                                                                                                                 202 GACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAA 26:
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Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
Royer, John
                                                                                             Hecht, Peter
Holtzman, Doug
                                                                         Madden, Kevin
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APPLICANT: Salama, Sofie
APPLICANY: Sherman, Amir
APPLICANY: Silva, Jeff
APPLICANY: Sliva, Jeff
APPLICANY: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 99/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PAtentin version 3.0
SEQ ID NO 426
LENGTH: 556
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-426
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Best Local Similarity:
Query Match:
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Search completed: February 25, 2003, 02:31:05 Job time : 33 secs
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                                                                                                                                                                                                                                                                       SerSerSerSerIleThrLeuSerSerGluHisThrThrValAspSerArgThr 282
                                                                                                                                                        AACTCTTCACCATCAACGACATTGTAGTAACATTCCTTGTTGACCGTGTCTTCAAAAACG
                                                                                                                                                                                                       SerSerThrThrSer----SerThrThrSerSerThrThrSerIlePheSerValThr
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                                                                                   ATGTAGCAGTACTCCGTCTTGAAACATGTTTTTTTGCATTCGTCA 147
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36.00%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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40.2
40.2
39.6
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45.8
45.8
45.2
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375
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                               Description
                                     DNA encoding novel Human p160 cDNA 16 Human p160 cDNA 16
                                                                                                                                                       Murine LOBO genomi
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|                              |               |           |              |   | _           |  |            |             |             |                            |            |                      |        |                                  |                  |              |                  |                    |                    |                      |                |        |  |                  |                |                    |                |                 |                  |                      |          |         |        |
|------------------------------|---------------|-----------|--------------|---|-------------|--|------------|-------------|-------------|----------------------------|------------|----------------------|--------|----------------------------------|------------------|--------------|------------------|--------------------|--------------------|----------------------|----------------|--------|--|------------------|----------------|--------------------|----------------|-----------------|------------------|----------------------|----------|---------|--------|
| PR<br>PR                     | PF            | PD        | PN           | FT FT FT                                    | 20          | XX KW XX                               | DE >       | DI          | <b>3</b> 83 | RESULT<br>AAA281<br>ID A   |            |                      |        |                                  | ۵                |              |                  | o<br>              | ta te              | a (4) (              | ωN             | NN     |  | α<br>2 2 1       | N N            |                    |                |                 |                  | 000                  |          |         |        |
| 18-M<br>12-M                 | 10-M          | 28-SI     | W0200        | Key<br>CDS                                  | Hirudo      | Saratin;  <br>collagen-<br>posterior   | Platelet   | 29-JA       | AAA28180    | ILT 1<br>28180<br>AAA28180 |            | 44                   |        |                                  |                  |              |                  |                    |                    |                      |                |        |  |                  |                |                    |                |                 |                  |                      |          |         |        |
| 8-MAR-1999;<br>2-MAY-1999;   | 0-MAR-2000;   | -SEP-2000 | WO200056885- |   | o medi      | in; med<br>gen-dep<br>rior ca          |            | 9-JAN-2001  | 180;        | ហ                          |            | 37.2<br>37.2         |        |                                  |                  |              |                  |                    |                    |                      |                |        |  |                  |                |                    |                |                 |                  |                      |          |         |        |
|                              | 2             | •         | -A1.         | 77.72E                                      | medicinalis | medicinal<br>-dependent<br>r capsule ( | binding i  | (firs       |             | tandard;                   |            | 9.9                  | 9 .    | 9.9                              | 9.9              | 10.0         | 0.0              | 10.1 29            | . ω i              | 4.4                  | 5.5            | 50     | 100  | 0.6 3            | 0.0            | 0.6                | 0.6            | 0.0             |                  |                      |          |         |        |
| 99EP-0105530<br>99EP-0109503 | 000WO-EP02117 |           |              | Location/64375 /*tag= a /product= /note= "P | ·           | leech;<br>platel<br>opacifi            | inhibitor  | t entry)    |             | cdna;                      |            | 315<br>315           | 315    | 315<br>315                       | 315              | 3543         | 1622             | 44528              | 1448               | 400<br>963           | 234            | 654    | 354  | 2207 2<br>7507 1 | 3489 2         | 3489 2             | 1944 2         | 1944 2          |                  | 766 2<br>1944 2      |          |         |        |
| 5530.                        | 117.          |           |              | Qualif<br>"Sara<br>latele                   |             | 0.0                                    | or protein | 2           |             | 375 вр                     |            | 22 AAF<br>22 AAI     | 22 AAF | 22 AB <i>P</i><br>22 AB <i>P</i> | 22 ABA           | 22 AAH       | 23 AAS<br>21 AAA | 24 AB              | 21 AAC             | 23 AAS<br>23 AAS     | 23 AAS         | 3 AAS  | 3 AAS  | 9 AAV            | 4 ABA          | 1 AAA              | 2 AAIC         | 2 AAII          | 2 ABAS           | 2 AAIU<br>2 ABA4     | 2 AAI4   | 2 ABA3  | 2 ABA6 |
|                              |               |           |              | iers<br>htin"<br>et adhesion                |             | oembo<br>sion<br>ss.                   | ein Sarat  |             |             | •                          | ALIGNMENTS | AAK43555<br>AAI24342 | 17735  | 36403                            | 51452            | 62819        | 70213            | A03041             | 47605<br>90738     | AAS75460<br>AAS68580 | /546/<br>75455 | 71153  | 90677  | 73805<br>19941   | 3487           | 0290               | )4231<br>)2791 | 2874            | 4575             | AAI07812<br>ABA44123 | 7409     | 4288    | 7193   |
|                              |               |           |              |   |             | lic disease;<br>inhibition;            | 'n         |             |             |                            | S.         |                      |        |                                  |                  |              |                  |                    |                    |                      |                |        |  |                  |                |                    |                |                 |                  |                      |          |         |        |
|                              | S<br>S        | •         |              | inhibitor F                                 |             | ξ.                                     | encoding c |             |             |                            |            |                      |        |                                  |                  |              |                  |                    |                    |                      |                |        |  |                  |                |                    |                |                 |                  |                      |          |         |        |
|                              | J. S.         | ر<br>ال   |              | protein                                     |             | intraocular                            | CDNA seg   |             |             |                            |            | Probe                | Human  | Probe                            | Human            | Shrimp       | Plasmodium       | Liste              | Arabid<br>DNA en   | DNA en               | DNA en         | DNA en | DNA en   | KSHV L           | Kaposi         | Kaposi<br>Nucleo   | Probe :        | Probe #2807 for | Human 1          | Human k              |          | Probe # |        |
|                              |               | •         |              | •   |             | r tens;                                | ence.      | ,<br>,<br>, |             |                            |            | #14275               |        | #14869                           | breast<br>foetal | Shrimp white | smodium falcip   | Listeria monocytog | Arabidopsis thatia | encoding             | coding         | coding | encoding pencoding pencodi | ong uni          | i's sarc       | 's sarc<br>tide se | #2782 u        | #2807 fi        | 0etal<br>#2825 f | preast               | :16095 u | #12047  |        |
|                              |               |           |              |   |             |  |            |             |             |                            |            | for g                | marrow | for g                            | cell<br>liver    | spot         | alcipa           | novel              | novel              | novel                | novel          | novel  | ding novel   | que c            | oma-a<br>(nucl | oma-a<br>quenc     | sed t          | or g            | or ge            | cell                 | used t   | for g   | liver  |

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CC encoding Saratin, an expression vector comprising the DNA sequence, a CC immunospecific for Saratin, and methods for identifying Saratin agonists CC or antagonists. Saratin is useful for treating thromboembolic processes, CC or antagonists. Saratin is useful for treating thromboembolic diseases. CC It is useful for preventing thromboembolic diseases. CC or coating artificial surfaces, since use of Saratin is also useful con-adhesive for cells and prevents the activation of cells. It may also useful for modifying intraocular lenses in order to lessen the CC useful for modifying intraocular lenses in order to lessen the CC useful for modifying to modify the lens material. For contacting the lens material is covalent crosslinking to modify the lens material. The lens material which may be implanted into the eye. This new type of coating avoids CC medicaments that are for instance conferring cell death, Saratin coating the lens to completely overcome nosterior cansule constitution with other helps to completely overcome nosterior cansule constitution with other helps to completely overcome nosterior cansule constitution with other helps to completely overcome nosterior cansule constitution which other helps to completely overcome nosterior cansule constitution which other the constitution with other material coating avoids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
       361
                                              361 GTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 375 BP; 123 A; 62 C; 85 G; 105 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  helps to completely overcome posterior capsule opacification. The antibody immunospecific for Saratin, as well as Saratin itself, are useful for measuring samples derived from host cell cultures or from a treated subject. The present sequence represents cDNA encoding the
                                                                                                                                                                              241 GGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTG
                                                                                                                                                                                                                            241 GGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTG 300
                                                                                                                                                                                                                                                                           181 TACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGAT 240
                                                                                                                                                                                                                                                                                                     181 TACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                   121 AAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saratin is a protein isolated from the saliva of the medicinal leech Hirudo medicinalis. Saratin is an inhibitor of collagen-dependent platelet adhesion. The invention includes polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 40; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Saratin polypeptide and gene isolated from Hirudo medicinalis for blocking platelet adhesion, especially useful for treating or preventing thrombotic diseases, or for manufacturing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thromboembolic diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAAGTATTTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAAGTATTTCTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ьоса.
                                                                                                          ACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAA 360
GTTGATGAAGATTAA 375
                                                                             ACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAA 360
                                                                                                                                                                                                                                                                                                                                                                         TCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 375; DB 21; Length 375; Pred. No. 3.3e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 0; Gaps
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7333 ATTTTGAAGAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG 7392
                                       323 CAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes the murine LOBO protein described
                                                                                                                                                                                   263 AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 other;
                                                                                                                                                                                                                                                                                                           203 ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                   143 ATCTTGACGAATGCAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the same and have osteopathic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 69-97; 391pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-601320/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45.8; DB 20; Length 49999;
Pred. No. 0.011;
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Best Local Similarity 49.8%;
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel nucleic acids (1; designated LOBO (long proteins influencing bone development in mammals. The bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. proteins of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodise can be used in ethods of the state of the skull and have osteopathic activity. The methods and nucleic acid molecules, etc. are useful for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases animals, especially a transgenic mouse for the study of diseases are specially attansgenic mouse for the study of diseases. This sequence encodes the murine LOBO protein described a chondroplasia. This sequence encodes the murine LOBO protein described in the mathematical control of the study of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-601320/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosenthal A, Rump A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 161-189; 391pp; German
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     in the method of the invention.
                                                                                                                                                                                                                                                                                 9318 ATTTTGAAGAAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG 9377
                                                                                                                                                                                                                       143 ATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG 202
                                                                                                                                                             203 ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
                            ABL06114 standard; cDNA; 15935 BP
ABL06114;
                                                                                                                               323 CAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGATTAA 375
                                                                                                                                                                                         263 AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98DE-1013799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hess J, Aigner T, Wirth T;
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Score 45.8;
                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                             8; DB 20;
0.011;
                                                                                                                                                                                                                                                                                                                                                                                               Length 49999;
                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                             9497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S PD XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prosophila; developmental biology; cell signalling; insecticide;
                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ss.
                                                             ABQ54916
                                                                                                                                                                                                                                                                                                                                                                                                    Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2
XXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention capable of developmental biology and in elucidating cell signalling and useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO1840-ABL16175) and the encoded proteins sequences (ABLO1840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABB62011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 12824; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                               10250 TAATGATGGGGACGACGATGACGGAGATGACAATGAGGACGACGAGGATAACGA 10191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions -
                                                                                                                                                                                                                                                              10190 AGAAGATAATAATGACGACGAAGATGACGATGAAGACGACGAGGATGACGAAGAAGA 10131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15935 BP; 4219 A; 3351 C; 3394 G; 4971 T; 0 other;
                                                                                                                                                                                             10130 CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA 10071
                                                                                                                              10070 AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 10017
                                                                                                                                                                                                                                                                                                                                                                 141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
                                                                                                                                                                                                                               261 AAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGA 320
                                                                                                                                                                                                                                                                                                201 AGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGA 260
                                              ABQ54916 standard; cDNA; 2438 BP
             ABQ54916;
                                                                                                                                                              321 TGCAGGTAATGCGGCAGGTACAGGTGACGAGGTCAGATGAAGTTGATGAAGATTA 374
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; Score 45.2; DB 49.6%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Length 15935;
                                                                                                                                                                                                                                                                                                                                                                                                                              118;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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22-AUG-2002 (first entry)

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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP4328) and to cDNAs encoding them (ABC54131-ABC56305), and also to the sequences of the invention. The invention additionally relates to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen contracting, prognosing or preventing various ovarian antigen antigen polynucleotides, antibodies against human ovarian antigens and the use of covarian antigen polynucleotides and polypeptides in diagnosing, conditions include ovarian cancer and breast-related disorders. Such conditions include ovarian cancer and breast-related conditions (e.g., infertility, disorders of pregnancy, annovulation, conditions (e.g., chlamydia, HIV, toxoplasmosis, endocrine ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine conditions (e.g., chlamydia, HIV, toxoplasmosis, endocrine conditions (e.g., antended disorders, and toxic conditions (e.g., mastitis, ophoritis, and toxic conditions (e.g., mastitis, ophoritis and corder conditates, autolumnue ophoritis, systemic lupus erythematosus), and urinary system disorders (e.g., antended ophoritis, systemic lupus erythematosus), conditate ovarian antigen pohypeptides and toxorders (e.g., antended ophoritis, systemic lupus erythematosus), conditate ovarian antigen pohypeptides and disorders, particular disorders, ophoritis, systemic lupus erythematosus), conditate ovarian antigen pohypeptides and conditate ovarian antigen pohypeptides and sourcers (e.g., chlamydia, cardiovascular disorders, conditate ovarian antigen pohypeptides and toxorders ophoritis, cardiovascular disorders, conditated ovarian antigen pohypeptides may be used as food additives or to prepare antibodies convention.
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2438 BP; 561 A; 761 C; 686 G; 427 T; 3 other;
                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                               specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 796; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABP41839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; inflammatory condition; immune disorder; blood disorder; unfection; cardiovascular disorder; respiratory disorder; peurological disorder; gastrointestinal disorder; respiratory disorder; neurological disorder; gene therapy, chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200200677-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                         The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian antigen HNBVO53 cDNA, SEQ ID NO:796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-147878/19.
                         11.8%;
Score 44.4; DB 24; Length 2438;
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polynucleotide are also used in diagnostics, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags (CC intestore normal activity of (II) or to treat disease states involving CC quantitating a polypeptide in tissue, as molecular weight markers and as CC quantitating a polypeptide in tissue, as molecular weight markers and as CC disorders involving aberrant protein expression or biological activity. (CC disorders involving aberrant protein expression or biological activity. CC disorders involving aberrant protein expression or biological activity. CC algorities, forensics, gene mapping, identification of mutations in cresponsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XX
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 11256; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG11265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-мак-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 52.1 Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #11256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS75452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS75452 standard; cDNA; 372 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1771 GGAAGAAGAA 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1651 AGAGGAAGAGGAAGACTTTGAGGAAGAGGAAGAGGATGAAGAGGAATATTTTGAAGA 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 TGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 CTGCGAGGGTAAAGATGCAGGTAATGCGGCGAGGTACAGGTGACGAGTCAGATGAAGTTGA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 AGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 CTACATGGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-639362/73.
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"'^mm+ches 91; Indels
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밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. AASG4197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 372 BP; 194 A; 27 C; 134 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT89346 standard; cDNA; 3211 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTC 210
                                                                                                                                                                                                                                                                                                                                                                                               p160; p62; cytoplasmic; T cell; B cell; development; activation; modulation; cellular response; cell proliferation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT89346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 GCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 GTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human p160 cDNA 160.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p56-lck; ss
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                 26-JUN-1997.
                                                                                                                                                                                                                                                         W09722255-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 10.9%;
Local Similarity 48.9%;
                                    cDNA encoding p62 and p160 and corresponding proteins – used in the treatment of autoimmune disease and for T and B cell prolliferation, e.g. for treatment of tumours \,
                                                                                                                                                                                                        11-DEC-1996;
                                                                                                                                                     (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                 19-DEC-1995;
            Claim 82; Fig 10; 175pp; English
                                                                                                                            Joung I,
                                                                                        P-PSDB; AAW31186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATCCCATAAACGGGAGTTCGAGACTCACCTAGGCAACATAGCGAAACCCCATCTGAAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-341351/31.
                                                                                                                              shin J, Strominger JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                  95US-0574959
                                                                                                                                                                                                             96WO-US19944
                                                                                                                                                                                                                                                                                                                          439..3156
                                                                                                                                                                                                                                                                                   /product= p160
/note= "160.2"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 23
Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 115; Indels
                                                                                                                                      Vadlamudi RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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8888888888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This cDNA sequence encodes a novel p160 (160.2) which is capable of activating transcription of a variety of genes upon activation of p62 of activating transcription of a variety of genes upon activation of p62 of is capable of binding to the p62/p561pk complex to modulate Lok and is capable of binding to the p62/p561pk complex to modulate Lok function in a manner similar to p62. The genes transcribed in T or B cell p160 activation likely include those of which are involved in T or B cell activation or production of T or B cell appending the production of T or B cell specific factors e.g. lymphokines or antibodies. This p160 B cell specific factors e.g. lymphokines or antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           place polypeptides can modulate degradation of cellular proteins e.g. cell pycle regulatory proteins stimulating expression of cell cycle dependent kinase inhibitors and arresting cell cycle progression at specific kinase inhibitors and arresting cell cycle progression at specific boundaries to thereby modulate cell proliferation. As place boosts B cell boundaries to thereby modulate cell proliferation. As place boosts B cell infections in the second control of the second control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide is also a substrate for serine/threonine kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3211 BP; 649 A; 990 C; 948 G; 624 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple sclerosis allergic reactions, Crohn's diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT89345 standard; cDNA; 3901 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p160; p62; cytoplasmic; T cell; B cell; development; activation; modulation; cellular response; cell proliferation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT89345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human p160 cDNA 160.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 GAAAAATTTGTTGGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p56-lck; ss.
                                                                                                                                                                                                                                                                                                                                                  WO9722255-Al.
                                                                                                                                                                          19-DEC-1995;
                                                                                                                                                                                                                               11-DEC-1996;
                                                                                                                                                                                                                                                                                    26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
WPI; 1997-341351/31
                                                    Joung I,
                                                                                                            (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
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                                                       Shin J, Strominger JL, Vadlamudi RK;
                                                                                                                                                                                 95US-0574959.
                                                                                                                                                                                                                                         96WO-US19944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439..3846
                                                                                                                                                                                                                                                                                                                                                                                                          /product= p160
/note= "160.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%; Score 40.2; DB 18; Length 3211; 52.0%; Pred. No. 0.17;
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P-PSDB; AAW31185.

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DT

DX

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PR
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        21-SEP-2000;
27-SEP-2000;
                                                         30-JUN-2000;
03-AUG-2000;
                                                                                                                04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                          30-JAN-2001;
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                                                                                                                                                                                                                                                                                                     WO200157271-A2.
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                      Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human breast cell single exon nucleic acid probe #7974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA49279 standard; DNA; 766 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3148 GAAGAAGAGGAAGAAGAGGAAGAGGGAAGACTTTGAGGAAGAGGAAGAAGAAGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cycle regulatory proteins stimulating expression of cell cycle dependent kinase inhibitors and arresting cell cycle progression at specific boundaries to thereby modulate cell proliferation. As p160 boosts B cell infections by pathogenic microorganisms, p160 can be used to expand T cell populations for treating infectious diseases or cancer and p160 thibitors could reduce B or T cell responses and may be used to treat a militial and contains and could reduce be cell infectious diseases or cancer and p160 thibitors could reduce B or T cell responses and may be used to treat a militial and could reduce B or T cell responses and may be used to treat a militial and could reduce B or T cell responses and may be used to treat a militial and could reduce B or T cell responses and may be used to treat a militial and could reduce B or T cell responses and may be used to treat a militial and could reduce B or T cell responses and may be used to treat a militial and could reduce B or T cell responses and may be used to treat a militial could reduce B or T cell responses and may be used to treat a militial could reduce B or T cell responses and may be used to treat a militial could reduce B or T cell responses and may be used to treat a militial could reduce B or T cell responses and may be used to treat a militial could reduce B or T cell responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial responses and may be used to treat a militial respon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA sequence encodes a novel p160 (160.1) which is capable of activating transcription of a variety of genes upon activation of p62 and is capable of binding to the p62/p561pk complex to modulate Lck function in a manner similar to p62. The genes transcribed in response to development/differentiation, T or B cell activation or production of T or B cell specific factors e.g. lymphokines or antibodies. This p160 polypeptide is also a substrate for serine/threenine kinase activity. P160 polypeptides can modulate degradation of cellular proteins e.g. cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3901 BP; 781 A; 1183 C; 1128 G; 809 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 GAAAAATTIGTIGTGGACGAAAACTICACGGAAAATTATTIGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple sclerosis allergic reactions, Crohn's diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
                                                                                                       2000US-0180312
2000US-0207456
                                                                                                                                                                                       2001WO-US00662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%; Score 40.2; DB 18; 52.0%; Pred. No. 0.18;
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PN XX

Homo sapiens.

WO200157277-A2

Human; foetal liver; gene expression; single exon nucleic acid probe;

Human foetal liver single exon nucleic acid probe #15498.

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BXI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the probes with a collection of detectally labeled nucleic acids collectived from mRNA of human breast, and then measuring the label collectived from the probes of the microarray. The probes are useful for collection of regions of genomic DNA predicted to determining predisposition and/or prognosing breast disease. Gene collective of expression analysis is useful for assessing the toxicity of chemical collective of eagents on cells. The microarray of this invention presents a far greater collective of probes for measuring gene expression, with far less bias crapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Collective than expressed atta for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                 01-FEB-2002 (first entry)
                                                                                  ABA67193 standard; DNA; 766 BP
                                                            ABA67193;
                                                                                                                                                                           507 GA 506
                                                                                                                                                                                                                      Sequence 766 BP; 190 A; 299 C; 36 G; 241 T; 0 other;
                                                                                                                                                                                                           367 GA 368
                                                                                                                                                                                                                                                     307 TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                                                                                                                                                                                     627 GĀTGGAĞAGGATĞATAATBATĞATĞACGATGATGATGATTATGATAATGATGGGGAGGAG 568
                                                                                                                                                                                                                                                                                                                   247 GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC 306
                                                                                                                                                                                                                                                                                                                                                     187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID NO 7974; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 10.6%;
Similarity 51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39.6; DB Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                           89; Indels
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RESULT 11
ABA34288/c
ID ABA342:
XX ABA342:
XC ABA342:
XX Probe
DF 23-JAN
XX Probe
XX Cardio
KW Cardio
KW Congen
XX Congen
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                   Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 15498; 639pp + sequence listing; English.
                                              Homo sapiens
                                                                         congenital heart
                                                                                                                           Probe #12754 for gene expression analysis in human heart cell sample.
                                                                                                                                                           23-JAN-2002
                                                                                                                                                                                      ABA34288;
                                                                                                                                                                                                                ABA34288 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 766 BP; 190 A; 299 C; 36 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     687
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                                                                                                                                                                                                                                                                                                                                                               307 TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                              GA 368
                                                                                                                                                                                                                                                                                                                                                                                           GATGGAGAGGATGATAATAATGATGACGATGATGATGATTATGATAATGATGAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
93; Conserv
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                         (first entry)
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2000US-0207456.
                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
                                                                                                                                                                                                                DNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥,
                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39.6; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                366
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RESULT 12
AA122114/c
ID AA1221
XX AA1221
XX AA1221
XY Probe
XX Probe;
KW Probe;
KW Probe;
KW Cervic
XX OS Homo s
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                            Probe; human; microarray;
cervical cancer; ss.
                                                                                                                                                       AAI22114 standard; DNA; 766
  Homo sapiens
                                                                      Probe #12047
                                                                                                12-OCT-2001
                                                                                                                             AAI22114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 766 BP; 190 A; 299 C; 36 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; IdM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                    187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                          GA
                                                                                                                                                                                                                                                    GA 368
                                                                                                                                                                                                                                                                               TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGGTCAGATGAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-488899/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG
                                                                                                                                                                                                                                                                                                                                                             GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC 306
                                                                                                                                                                                                                                                                                                                                                                                          TCCACACTTGAGGACAACCATGAGGATGATGATGATGAAGATGAAGATGATGGTGGT 628
                                                                                                                                                                                                                                                                                                                                     GATGGAGAGGATGATAATAATGATGACGATGATGATGATATGATAATGATGGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon nucleic acid probes for analyzing gene expression in human \ddot{\phantom{a}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                     for gene expression analysis in human cervical cell sample
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID No 12754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.6%;
51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530pp; English.
                                                                                                                                                       ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39.6; DB.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.14
); Mismatches
                                         expression; cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 88
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Indels Length

Gaps

0;

568

766; 0;

epithelial cell;

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RESULT 13
AAI47409/c
ID AAI474
XX AAI474
AC AAI474
XX AAI474
XX Probe;
KW Probe;
KW geneti
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                           (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID No 12047; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
          genetic
                    Probe; microarray; human;
                                        Probe #16095 used to measure
                                                             17-OCT-2001
                                                                                                     AAI47409 standard;
                                                                                                                                                                                                                                                                                                                                                               Sequence 766 BP; 190 A; 299 C; 36 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-)
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                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                         GA
                                                                                                                                                                                                                                                                                                    TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                             GA
                                                                                                                                                                                                 TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT
                                                                                                                                                                                                                                         GATGGAGAGGATGATAATAATGATGACGATGATGATGATTATGATAATGATGGGGAGGAG
                                                                                                                                                                                                                                                            GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAAATTATTTGACAGAC 306
                                                                                                                                                                                                                                                                                 2001-488901/53
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                                                                                                                                                                            368
                                                                                                                                                                                                                                                                                                                                  Similarity
           disorder;
                                                                                                                                                         506
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-06323687.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US00670
                                                             (first
                                                                                                      DNA;
                                                            entry)
                                                                                                                                                                                                                                                                                                                                  10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                    placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                  Score 39.6; DB Pred. No. 0.14;
                                      gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR
                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                        89;
                                                                                                                                                                                                                                                                                                                                           Length 766;
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RESULT 14
AAIO7812/G
ID AAIO7
XX AAIO7
XX AAIO7
XX AAIO7
XX D9-OC
XX Probe
XX Probe
XX Probe
XX Probe
XX Probe
XX Homo
OS Homo
ON WO200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
                                                                                                          Probe #7803 used to measure gene expression in human breast sample
                                                                                                                                     09-OCT-2001
                                                                                                                                                               AAI07812;
                                                                                                                                                                                         AAI07812 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 766 BP; 190 A; 299
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                                                                  inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                        sapiens
                                                                                                                                                                                                                                                             GA:
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                                                                                                                                                                                                                                                                                                                                                                     GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAAATTATTTGACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                         TCCACACTTGAGGACAACCATGAGGATGATGGTGATGAAGATGAAGATGATGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single
                                                                                human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                           506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                   disease;
                                                                                                                                    (first
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                                                                                breast disease; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No 16095; 654pp;
                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%;
51.1%;
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                                                                   proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 36 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon nucleic acid
n human placenta –
                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39.6; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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                                                                   breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR;
                                                                  cancer; develo
breast disease;
                                                                                development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                    non-carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       766;
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WO200157270-A2

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RESULT 15
ABA44123/c
ID ABA4411
XX ABA4411
XX
AC ABA441
XX
DT 01-FEB
XX DE Human |
XX Human;
KW diseas,
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                    Human breast cell single exon nucleic acid probe #2818.
                    Human; microarray; single exon probe; gene expression; breast;
                                                                                                                         ABA44123
                                                                                          01-FEB-2002
                                                                                                                                                  ABA44123 standard; DNA; 1944 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases of the breast cancer, disorders of development, inflammatory diseases of the breast, fiborocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 766 BP; 190 A; 299 C; 36 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for
                                                                                                                                                                                                                                507 GA 506
                                                                                                                                                                                                                                                             367 GA 368
                                                                                                                                                                                                                                                                                Novel single exon nucleic acid probe used to measuring gene expression in a human breast .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                           307 TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                                                                                                                                                                                                                                                                        247 GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC 306
                                                                                                                                                                                                                                                                                                                                                                                                      187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                           GATGGAGAGGATGATAATAATGATGACGATGATGATGATTATGATAATGATGGGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 7803; 322pp; English.
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2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid probes for measuring gene expression in a sample derived CC from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC werifying the expression of regions of genomic DNA predicted to CC encode proteins. They are useful for gene discovery, and for CC encode proteins. They are useful for gene discovery, and for CC determining predisposition and/or prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater CC diversity of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for crapid production of functional information from genomic sequence. The CC present sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                              Sequence 1944 BP; 466 A; 599 C; 349 G; 530 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 2818; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid probes useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                           804 GACGAGGAGAATGATGGTGATAGT,GGTGATGATGAAAATGATGATGAGGAGAATGAGGAT 745
                                                                                                                                                                                                                                            187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
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744 GA 743
                                367 GA 368
                                                                                              307 TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                                  864 GATGGAGAGGATGATAATAATGATGACGATGATGATGATTATGATAATGATGGGGAGGAG 805
                                                                                                                                                                       247 GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC 306
                                                                                                                                                                                                            from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                            Local Similarity
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| 33.2              | 33.4              | 33.4              | 33.4               | 33.6              | 33.6              | •                 | 33.6              |                   | 33.6              | 33.8              | 34                | 34                | 34                | 34                | 34                | 34                | 34                |
| 8.9               | 8.9               | 8.9               | 8.9                | 9.0               | 9.0               | 9.0               | 9.0               | 9.0               | 9.0               | 9.0               | 9.1               | 9.1               | 9.1               | 9.1               | 9.1               | 9.1               | 9.1               |
| 4599              | 1839              | 1727              | 1137               | 4080              | 4080              | 4080              | 2295              | 2295              | 2295              | 4518              | 980               | 980               | 980               | 980               | 980               | 980               | 759               |
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| US-08-431-080-27  | US-09-071-035-293 | US-09-071-035-295 | US-09-134-001C-657 | PCT-US95-16930-1  | US-09-177-431-1   | US-08-375-300-1   | PCT-US95-16930-3  | US-09-177-431-3   | US-08-375-300-3   | US-08-961-527-121 | PCT-US95-12414-3  | US-08-466-743-3   | US-08-466-717-3   | US-08-468-066-3   | US-08-314-503A-3  | US-08-466-603-3   | PCT-US95-12414-4  |
| Sequence 27, Appl | Sequence 293, App | Sequence 295, App | Sequence 657, App  | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 3, Appli | Sequence 3, Appli | Sequence 3, Appli | Sequence 121, App | Sequence 3, Appli | Sequence 4, Appli |

## ALIGNMENTS

US-08-232-463-14/c
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINEER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS

ADDRESSEE: Foley & Lardner Alexandria VA

1800 Diagonal Road,

Suite 500

STREET: CITY: A

COUNTRY: USA ZIP: 22313-0299

, CLONE: pTZgpt-F1s US-08-232-463-14 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: 606/4/3 683-4109 SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid ZIP: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: IMMEDIATE SOURCE: CLONE: pTZgpt-FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: U STRANDEDNESS: TOPOLOGY: lir APPLICATION NUMBER: linear single EP 91 114 300.6 US/07/935,313 US/08/232,463 30472/114 IMMU

Sequence

Query Match

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Score 42.2;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                           FEATURE
                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 3211 base pai
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DE TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-DEC-95
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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NAME: Mandragouras, Amv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                      NAME: Mandragouras, Amy E REGISTRATION NUMBER: 36,2
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                          02109-1875
                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                3211 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 State Street,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                             (617)227-5941
                                            CDS
439..3157
                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                         CDNA
                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p62 POLYPEPTIDES,
AND USES THEREFOR
10.7%;
                                                                                                                                                                                                                                                                                                                 US/08/574,959A
                                                                                                                                                                                                                                                      36,207
                                                                                                                                                                               8.
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                                                                                                                                                                                                                                          DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 510
Score 40.2;
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DB
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Length 3211;
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2458 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAACTTTGAAGAAGAAGAAGAAGATGAAGAA 2517

259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318

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GENERAL INFORMATION:
                                     Matches
                                                                    Query Match
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                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
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                                                 Local
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/574,959
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger
                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                       MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: p62 POLYPEPTIDES,
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                                     90;
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                            LENGTH: 3211 base pairs
                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
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                                   Conservative
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                                                 10.7%;
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                             Score 40.2; DB 4;
Pred. No. 0.0066;
""ematches 83;
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                                                                  Length 3211;
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RESULT 5
US-09-357-014-6
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US-08-574-959A-6
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         Sequence 6, Application US/09357014 Patent No. 6291645
                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                3148 GAAGAAGAGGAAGAAGAAGAAGAGGAAGACTTTGAGGAAGAAGAAGAAGATGAAGAG 3207
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DF TELECOMMUNICATION INFORMATION: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DDS/MS-DOS
OPERATING SYSTEM: PC-DDS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                   319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                   199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                           259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          439..3847
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US-08-728-323A-1
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                                                                                                                                                   Sequence 1, Application US/08728323A Patent No. 5948676
                                                                    GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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TITLE OF INVENTION:
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                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                   319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                              199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
FILING DATE: <0nknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE : ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 439..3847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
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STATE: Massachusetts
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                                    Edelman, Isidore S. Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Sarcoma-Associated Herpesvirus,
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               Immediate Early Protein From Kaposi's
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                                                                                                                                                                                     US-09-298-568-1
                                                     Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
               TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                         1111 GAGGATGACGAGGA 1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                               358 GAAGTTGATGAAGA 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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1185 Avenue of the Americas
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 Mismatches

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Best Local Similarity
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CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chang, Yuan
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TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. 28,678
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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ADDRESSEE: Cooper & Dunham LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 ZIP:
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Edelman, Isidore S.
Moore, Patrick S.
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RESULT 9
US-08-757-669A-20/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 20, Application US/08757669A Patent No. 6183751
              TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chang, Yuan
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Best Local Similarity
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                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
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APPLICANT:
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                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                            NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
   LENGTH:
                                                                                               REFERENCE/DOCKET NUMBER: 45185-F
                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                    APPLICATION NUMBER: US/08/757,669A
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                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
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TOPOLOGY: li
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nucleic acid
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1185 Avenue of the Americas
32207 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isidore S.
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US-09-230-371A-20/c
Sequence 20, Application US/09230371A
Patent No. 6348586
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APPLICANT:
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                                       21006 GATGAGGAGCAGGAGACAGATGAGGAGGACGAGGATGACGAGGAGGATGACGAG 20947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/230,371A CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: PCT/US97/13346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 45185-G-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 120;
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                                                                                                                       21066 GGGGACAACGAGATTAGCAAGGAAAGTCAGGTTGACAAGGATGACAATGACAATAAGGAT 21007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                       21126 GAAGAAGCATCCAAGAATGAAAAAGAATGTTCCGAAAATAATCAGGCTGGCGAGGATAAT 21067
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Kaposi's sarcoma-associated herpesvirus
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TOPOLOGY: lin
MOLECULE TYPE:
298 TTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGAT 357
                                                                                                                                                                178 GAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTT 237
                                                                                238 GATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTAT 297
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                                                                                                                                                                                                                                                                                                                        Local Similarity
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Moore, Patrick S
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RESULT 11
US-08-766-738-2
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APPLICANT: BANDMAN, Olga
APPLICANT: GOLI, SUTYA K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                      Query Match
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IMMEDIATE SOURCE:
LIBRARY: Consen:
CLONE: 1813361
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                                                                                                                                                                                          583 GTTGATNAAGANGAGGAGGACGGAGAAGGAGAGAGAGGAGGAGGACGATGAGGAT 642
                                                                                                                                                                                                                              193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
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STREET: 31
                                                                  313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                   643 GGTGAAGAAGAGGAGTTTGATGAAGAAGATGATGAAGATGAAGATGTAGAAGGGGATGAG 702
                                                                                                                                                       253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
                                         703 GACGACGATGAAGTCAGTGAGGAAGGAAGAATTTGGACTTGATGAAGAAGATGAAGAT 762
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       373 TA 374
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                                                                                                                                                                                                                                                         9.6%; Score 36; DB 2; Length 966; Local Similarity 49.5%; Pred. No. 0.077; Local Similarity 0; Mismatches 92: Tracin
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
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3174 Porter Drive
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US-08-867-941-2
                 RESULT 13
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Best Local
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CORRESPONDENCE ADDRESS:
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LIBRARY: Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
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                                                                                                                                               703 GACGACGATGAAGTCAGTGAGGAGGAAGAAGTTTGGACTTGATGAAGAAGATGAAGAT 762
                                                                                                                                                                                    313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAAGTTGAAGTTGAAGAT 372
                                                                                                                                                                                                                          643 GGTGAAGAAGAGGAGTTTGATGAAGAAGATGAAGATGAAGATGTAGAAGGGGATGAG 702
                                                                                                                                                                                                                                                           253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
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                                                                        763 GA 764
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                                                                                                                         Patent No.
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                                                                                                    GENERAL INFORMATION:
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9.3%;
Best Local Similarity 52.2%;
                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 105; Conservative
                  APPLICANT: Run-pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFF
                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (416) 595-1163

SEQUENCE CHARACTERISTICS:
LENGTH: 2694 base pairs
                                                                                                                                                                                                2191 TCACAAGATGATGACGCAGAT 2211
                                                                                                                                                                                                                                       2077 TATCTGTTAACCGAAGACTTCACCCCAGAA-----GATGATGACGATGATTTGACCGCA 2130
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ZIP: M5G 1R7
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC COmpatible
TOWNSTER: JEM PC PC-DOS/MS-DOS
TOWNSTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                     2017 AAAAAGGACAAAGGTTATAGCAATAATGAAGAAAACCATCAAGAAAAAAGGCCATCAAGAT 2076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: STRANDEDNESS: Sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 24,973
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: //16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LACTOPERRIN RECEPTOR GENES OF MORAXELLA NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS: AM MCBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE: 03-JUN
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stewart, Michael
REGISTRATION NUMBER: 2
                                                                                                                          Application US/09074658 6184371
                                                                                        Loosmore,
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Yang, Yan-Ping
Klein, Michel H
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Du, Run-Pan
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LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                                                     Sheena M
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COMPUTER READABLE FORM:
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                                                                             NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                  STREET: 6th rac
                                                                                                                           TITLE OF INVENTION:
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                                                     ADDRESSEE: 51...
ADDRESSEE: 51...
Charter 6th Floor, 3
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                2131 TCTGATGATTCACAAGATGATGATGCACATGGCGATGATGATTTGATTGCATCTGATGAT 2190
                                 COUNTRY:
                                               STATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                     M5G 1R7
                                                                                                                                                                                                               INFORMATION:
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                                             Ontario
                                                                                                                                    Wang, Quijun
Yang, Yan-Ping
Klein, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
DEDNESS: single
                              Canada
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6th Floor, 330 University Avenue
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                                                           330 University Avenue
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Page 8

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CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: MICHAEL I
NAME: Stewart, MICHAEL I
NAME: STEWART NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7650 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-867-941-1
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search completed: February 25, 2003, 01:50:29
Job time : 71 secs
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Best Local Similarity 52.2%; Pred. No. 0.42;
Matches 105; Conservative 0; Mismatches 90; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OFTWARE: PATCHTION DATA: CURRENT APPLICATION NUMBER: US/08/867,941 APPLICATION NUMBER: US/08/867,941 FILING DATE: 03-UN-1997
                                                                                                                                                                                                                                                                                                            ||| | || || || || || || || 2351
                                                                                                                                                         2271 TCTGATGATTCACAAGATGATGATGCACATGGCGATGATGATTTGATTGCATCTGATGAT 2330
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                                                                                                                   352 TCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                                                     292 AATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAG 351
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GenCore version 5.1.3 Coppyright (c) 1993 - 2003 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   |  |  |  |   |  |  |   |                     | 31                             |
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| 34.6                                      | 34.8                                   | 34.8<br>8  | 35.4<br>35                                 | 35.8<br>35.4                            | 36<br>35.8                             | 36<br>36                               | 39.6                                      | 39.6                | Score                          |
|   |  |  |  |   |  |  |   | 10.6                | Query<br>Match                 |
| 542                                       | 5361                                   | 563<br>327   | 1092<br>267                                | 474<br>876                              | 966<br>204                             | 381<br>381                             | 1944<br>315                               | 766                 | Query<br>Query<br>Match Length |
| 10  | ومو                                    | 10   | 9<br>10                                    | 10                                      | 10                                     | 10                                     | 10  | 10                  | DB                             |
| US-09-864-761-4988<br>US-09-864-761-12239 | US-09-742-096-2<br>US-09-742-096-1     | US-09-864-761-13293<br>US-09-864-761-28059<br>US-09-764-848-19 | US-09-938-842A-1125<br>US-09-878-574-15076 | US-09-864-761-4255<br>US-09-770-445-544 | US-10-213-700-2<br>US-09-864-761-21008 | US-10-015-219-700<br>US-09-777-564-700 | US-09-864-761-2825<br>US-09-864-761-21723 | US-09-864-761-19608 | ID                             |
| Sequence 4988, Ap<br>Sequence 12239, A    | Sequence 2, Appli<br>Sequence 1, Appli | Sequence 13293, A<br>Sequence 28059, A                         | Sequence 1125, Ap<br>Sequence 15076, A     | Sequence 4255, Ap<br>Sequence 544, App  | Sequence 2, Appli<br>Sequence 21008, A | Sequence 700, App<br>Sequence 700, App | Sequence 2825, Ap<br>Sequence 21723, A    | Sequence 19608, A   | Description                    |

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|---|---|---|--|---|
| 443   | 38<br>39<br>40<br>41  | 35<br>35<br>36  | 32<br>32<br>32<br>32   | 222222<br>26543<br>26543  |
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| 5711<br>5711<br>5711<br>5711                          | 1959<br>2920<br>5711<br>5711<br>5711  | 7657<br>157<br>423<br>58985   | 1824<br>305<br>496<br>420<br>451<br>451  | 8391<br>8493<br>846<br>1282<br>381<br>659158  |
| 9999  | 10<br>9<br>9  | 10<br>9<br>9  | 100100100  | 10  |
| US-09-982-828-3<br>US-09-982-828-5<br>US-10-022-819-1 | US-09-864-761-4012<br>US-09-801-574-87<br>US-09-734-672-1<br>US-09-734-672-3<br>US-09-734-672-5<br>US-09-734-672-5          | US-09-070-927A-33<br>US-09-864-761-29856<br>US-09-938-842A-592<br>US-09-901-152-3 | US-09-864-761-1252<br>US-09-864-761-1252<br>US-09-864-761-2534<br>US-09-864-761-3256<br>US-09-864-761-554<br>US-09-864-761-14152 | US-10-151-736-3<br>US-10-151-736-5<br>US-09-815-242-8918<br>US-10-002-344A-89<br>US-09-864-761-21610<br>US-09-8771-208-20<br>US-09-815-242-9281 |
| μ,ς,ω,  | Sequence 4012, Ap<br>Sequence 87, Appli<br>Sequence 1, Appli<br>Sequence 3, Appli<br>Sequence 5, Appli<br>Sequence 5, Appli | Sequence 33, Appl<br>Sequence 29856, A<br>Sequence 592, App<br>Sequence 3, Appli  | Sequence 19262, A<br>Sequence 19262, A<br>Sequence 2534, Ap<br>Sequence 25266, A<br>Sequence 6554, Ap<br>Sequence 14152, A       | Sequence 3, Appli<br>Sequence 5, Appli<br>Sequence 8918, Ap<br>Sequence 89, Appl<br>Sequence 21610, A<br>Sequence 20, Appl<br>Sequence 9281, Ap |

## ALIGNMENTS

| PRIOR FILING DATE: 2001-01-30  PRIOR APPLICATION NUMBER: PCT/US01/00668  PRIOR APPLICATION NUMBER: PCT/US01/00663  PRIOR FILING DATE: 2001-01-30  PRIOR FILING DATE: 2001-01-30  PRIOR FILING DATE: 2001-01-30  PRIOR APPLICATION NUMBER: PCT/US01/00661  PRIOR APPLICATION NUMBER: PCT/US01/00661  PRIOR PILING DATE: 2001-01-30 | TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL; FILTE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: ACONIGA-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR PILING DATE: 2000-08-03 PRIOR PILING DATE: 2000-10-04 | RESULT 1  US-09-864-761-19608/c  Sequence 19608, Application US/09864761  ; Patent No. US20020048763A1  ; GEMERAL INFORMATION:  APPLICANT: Penn, Sharron G.  ; APPLICANT: Rank, David K.  ; APPLICANT: Hanzel, David K.  ; APPLICANT: Chen, Wensheng |
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APPLICANT:
APPLICANT:
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SOFTWARE: Annomax Sequence
SEQ ID NO 19608
LENGTH: 766
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                     PRIOR
                                                                                                                                                                                        PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                       FILE REFERENCE: Aeomica-X-1
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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OTHER
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ORGANISM: Homo sapiens
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                                                                     FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
                                                                                                                            APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                   APPLICATION NUMBER: US (FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GA 506
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                                                                                                                                                                                                                                                                                                                           Hanzel, David K.
Chen, Wensheng
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NN: EXPRESSED IN BT474, SIGNAL = 1.1

NN: EXPRESSED IN HELACENTA, SIGNAL = 1.1

NN: EXPRESSED IN HELLOO, SIGNAL = 1.1

NN: EXPRESSED IN HELA, SIGNAL = 1.1

NN: EXPRESSED IN HEAT, SIGNAL = 1.2

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

NN: SWISSPROT HIT: P17164, EVALUE 4.10e+00

NN: EST_HUMAN HIT: AW844901.1, EVALUE 2.90e+00
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                                                     US 60/236,359
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Pred. No. 0.05
0; Mismatches
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0.051;
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng

FILE REFERENCE: Aeomica-X-1

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

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US-09-864-761-21723

; Sequence 21723, Application US/09864761

; Patent No. US20020048763A1
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Best Local
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LENGTH: 1944
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
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                                                                                                                                                                                                                                                                                                                     247 GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC
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                                                                                                                         744 GA
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

2001-05-23

PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04

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Best Local
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OTHER
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ORGANISM: Homo sapiens
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                  310 GAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAA
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                                                                                                                                                                            190 ATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAG 249
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                                                                                                                                                                                                                                        Local Similarity
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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Conservative
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N: EXPRESSED IN BONE MARROW, SIGNAL = 2.3

N: EXPRESSED IN HBL100, SIGNAL = 2.9

N: EXPRESSED IN PLACENTA, SIGNAL = 2.9

N: EXPRESSED IN HEART, SIGNAL = 2.6

N: EXPRESSED IN LUNG, SIGNAL = 2.5

N: EXPRESSED IN HELA, SIGNAL = 2.6

N: EXPRESSED IN HELA, SIGNAL = 2.9

N: EXPRESSED IN BRAIN, SIGNAL = 2.9

N: EXPRESSED IN HELA, SIGNAL = 2.9

N: EXPRESSED IN HELA, SIGNAL = 2.6

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
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93; Indels
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US-09-783-590-5790
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEO ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William A.
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LOCATION: (302)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g,
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                                                      NAME/KEY: misc feature LOCATION: (348)
                                                                                                               NAME/KEY: misc feature LOCATION: (346)
                                                                                                                                                     OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                            OTHER INFORMATION: n equals
                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (337)
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NAME/KEY: misc feature LOCATION: (368)
                                    OTHER INFORMATION: n equals a,t,g, or
                                                                                           OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                         LOCATION: (345)
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; OTHER INFORMATION: n equals a,t,g, or US-09-783-590-5790
 Query Match
                                                                                                LOCATION: (492)
OTHER INFORMATION: n equals a,t,g,
                                                                        NAME/KEY: misc feature LOCATION: (497)
                                                                                                                                              NAME/KEY: misc feature
                                                                                                                                                         OTHER INFORMATION: n equals a,t,g,
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LOCATION: (476)
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (408)
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Length 499;

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RESULT 6
US-09-777-564-700
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 66, 201, 213, 225, 251,
LOCATION: 313, 322, 339, 373
COHER INFORMATION: n = A,T,C or G
US-10-015-219-700
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                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                 Sequence 700, Application US/09777564 Patent No. US20020022591A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 700, A Publication No.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
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CURRENT FILING DATE: 2002-03-02
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                                                                                                                                                                                                                                                                                                                                                                                                   313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                                                                                                                                                        201 NA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GTGGATGAAGAGGAGGAGGACGAAGAAGAAGATGAGGAAGACNAGGACGATGAGGAT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GGTGAAGAAGAGGAGTTTGATGAAGAAGATGATGAAGATGAAGATGTAGAAGGGGGATGAG
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Similarity 49.5%;
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Pred. No.
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NAME/KEY: misc_feature

LOCATION: (1)...(381)

OTHER INFORMATION: n = A,T,C or G

US-09-777-564-700
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LENGTH: 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
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                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0177 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            APPLICATION NUMBER: US/08/766,738
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO11, SUTYA K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/213,700 FILING DATE: 06-Aug-2002 CLASSIFICATION: CUnknown>
TYPE: nucleic acid
                                                                                      TELEPHONE: 415-855-05
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: CA
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                                                                                                         415-855-0555
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Pred. No.
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US-09-864-761-21008/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                            PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                 PRIOR EPLICATION NUMBER: PCT/US01/00667
PRIOR ETLING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                              PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00664 PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 GGTGAAGAACAGGAGTTTGATGAAGAAGATGATGAAGATGAAGATGTAGAAGGGGATGAG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          583 GTTGATNAAGANGAGGAGGACGGAGAAGGAGGAGAAGATGAGGAAGACGAGGACGATGAGGAT 642
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APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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l Similarity 49.5%;
90; Conservative
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Pred. No. 0.61;
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US-09-864-761-4255/c
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                                                                                                                          TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 99/632,366 PRIOR PRIOR APPLICATION NUMBER: US 99/632,366 PRIOR APPLICATION NUMBER: US 99/632,366
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
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PRIOR APPLICATION NUMBER: US 60/236,359
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                                   FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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R INFORMATION:
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R INFORMATION:
APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
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13; Conservative
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Hanzel, David K.
Chen, Wensheng
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EXPRESSED IN PLACES
EXPRESSED IN HEART
EXPRESSED IN FETAL
EXPRESSED IN BT474
EXPRESSED IN BRAIN,
EXPRESSED IN BONE N
EXPRESSED IN LUNG,
EXPRESSED IN HELA,
EXPRESSED IN HELA,
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IN FETAL LIVER, SIGNAL =
IN BT474, SIGNAL = 1.5
IN BRAIN, SIGNAL = 1.9
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RESULT 10 US-09-770-445-544/c

Sequence 544, Application US/09770445 Patent No. US20020023281A1

GENERAL

INFORMATION:

Gorlach, Jorn

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

An, Yong-Qiang Hamilton, Carol I Price, Jennifer I

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

APPLICANT:

Raines, Tracy M. Yu, Yang Rameaka, Joshua G. Page, Amy Matthew, Abraham V

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LENGTH: 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                            238 GATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTAT 297
338 GATGAAAATGAAGAT 324
                                             358 GAAGTTGATGAAGAT 372
                                                                                      298 TTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGAT 357
                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                      ER INFORMATION: MAP TO AL121580.6
ER INFORMATION: EXPRESSED IN PLACEN
ER INFORMATION: EXPRESSED IN HEART,
ER INFORMATION: EXPRESSED IN FETAL
ER INFORMATION: EXPRESSED IN BT474,
ER INFORMATION: EXPRESSED IN BRAIN,
ER INFORMATION: EXPRESSED IN BONE M,
ER INFORMATION: EXPRESSED IN HELA,
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FILING DATE: 2001-01-30
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ED IN HEART, SIGNAL = 1.4
ED IN FETAL LIVER, SIGNAL = 1.1
ED IN BT474, SIGNAL = 1.5
ED IN BRAIN, SIGNAL = 1.9
ED IN BONE MARROW, SIGNAL = 1.3
ED IN LUNG, SIGNAL = 1.6
ED IN LUNG, SIGNAL = 1.7
ED IN HELLA, SIGNAL = 1.7
ED IN HELLA, SIGNAL = 1.7
ED IN HELLA, SIGNAL = 1.7
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                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                       DB 10;
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                                                                                                                                                                                                                                                                                                         Length 474;
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APPLICANT: Hurban, Neith
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: Expressed Sequences of
FILE REFERENCE: 202US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/99/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
NUMBER OF SEQ ID NOS: 999
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 544
LENGTH: 876
TYPE: NNA
                                                                                               US-09-938-842A-1125
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US-09-938-842A-1125
Ouery Match 9.4%; Score 35.4; DB 9; Length 1092; Best Local Similarity 52.3%; Pred. No. 0.96; Matches 78; Conservative 0; Mismatches 71; Indels 0
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; ORGANISM: Arabidopsis thaliana
US-09-770-445-544
                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1125
                                                                                                                                                                                                                                                                                                                    APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE REFERENCE: SCRIP1300-3
CURRENT FALLIGATION NUMBER: US/09/938,842A
CURRENT APPLICATE: 2001-08-24
CURRENT FILLING DATE: 2001-08-24
DBTOD ADDITORMITON NUMBER: US/09/938,842A
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                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
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                                                                                                          TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 ACAATGATCTCGAAGCAGCTGATCTCGATGAAGATGGAGTTGTTGGAGCTGCAGAGTTTA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 CGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTG 346
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Allen, Keith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ledford, Brooke L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kricker, Maja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woessner,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Gaps
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-02-04
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
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LENGTH: 267
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701069621H1
US-09-878-574-15076
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                                                                                                                                                                                                      APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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       PRIOR
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FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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Patent No. US20020110548A1
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 GGAAAGGAGGATGAATCTGGTGATGATGATGACGATCAA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 GGTACAGGTGACGAGTCAGATGAAGTTGAAGATTAA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 ACGAGTCAGATGAAGTTGATGAAGATTAA 375
FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                            David K.
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Best Local 9
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                                                     GENERAL
                                                                   Sequence 28059, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: MAP TO AC012404.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                 APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 AAGTCCTCTGATCTTGACGAATGCAAAAAAAACATGTTTCAAGACGGAGTACTGCTACATC 192
                                                                                                                                                                                                                                                                                                                                                                                               131 TGTAAAGGATGGAAAAATGTAAAGGATGAATTAAAACAGTTCCACACGAAGAAGAAGAA 190
                                                                                                                                                                                                                                                     313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                                                                                                                                                                                              191
                                                                                                                                                                                                                                                                                                                                                             253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                  193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                                                                                     373 TAA 375
                                                                                                                                                                                  311 GAA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                            113;
                                                       INFORMATION:
Hanzel, David K.
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 28059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 2
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                                                                                                                                                                                                                                                                                                                  Query Match
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AC005668.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 327
                                                                                                                                                                                                                         217 GAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGAC 276
                                                                                                                                                                             320 GATGATGACAGCAGTGATGATGATGATGACAGCAGTGATGATGATGATGATGAGAAT 261
200 GATGATGATGATGACAGTGATGATGATGATGATGA
                                        337 GGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
                                                                                      260 GATGATGATGACAGTGATGATGACAGCGATGACAATGATGATGACAGTGATGAT 201
                                                                                                                                  277 GAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                   Local
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                   DB 10;
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Command line parameters:

-WODEL=frame+_n2p.model -DEV=xlh
-Q-/cgn2_f/USPTO_spool/US09936737/runat_14022003_100558_1407/app_query.fasta_1.519
-Q-/cgn2_f/USPTO_spool/US09936737/runat_14022003_100558_1407/app_query.fasta_1.519
-DB=PIR_73 -OFMT=fastan -SUFFIX=rpr -MINATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09936737_eCGN_1_1_16_grunat_14022003_100558_1407 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5 -FGAPOD=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                     Result
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                                                                                                                                                                                                                      Score
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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674
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 A36811
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|---|--------------------|---------------------------------------|-------------------------|--------------------|--------|--------|--------------------|--------|----------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------|--------------------|
| 44<br>45                                | 442<br>43          | 40<br>41                              | 3 6                     | 37                 | 36     | ω<br>5 | ω.                 | ယ္မ    | 32       | ω.     | 30                 | 29                 | 28                 | 27                 | 26     | 25     | 24     | 23     | 22     | 21     | 20     | 19     | 18                 | 17     | 16     | 15                 |
| 73.5<br>73.5                            | 73.5<br>73.5       | 73.5<br>73.5                          | 73.5                    | 73.5               | 73.5   | 74     | 74                 | 74     | <b>v</b> | 74.5   | 74.5               | 74.5               | 74.5               | 75                 | 75     | 75     | 75     | 75     | 75.5   | 75.5   | 76     | 76     | 76                 | 76.5   | 76.5   | 77                 |
|   | 10.9 $11.3$        |                                       |                         |                    | •      |        |                    | 11.4   |          |        | 11.4               | 11.1               | 11.1               | 11.1               |        | 11.5   |        |        |        |        | 11.3   |        |                    | 11.4   | 11.4   | 11.4               |
| 2339<br>4572                            | 562<br>636         | 357<br>562                            | 228                     | 222                | 208    | 4466   | 612                | 600    | 296      | 643    | 328                | 146                | 146                | 3844               | 2410   | 534    | 360    | 344    | 491    | 336    | 1278   | 1255   | 559                | 786    | 168    | 555                |
| NN                                      | N N                | 00                                    | 2 6                     | 2                  | N      | سر     | ν                  | N I    | N I      | ν      | Ν                  | ب                  | ப                  | N                  | Ν      | N      | N      | N      | 2      | N      | N      | N      | N                  | N      | N      | 2                  |
| A45597<br>S57908                        | \$50371<br>\$63131 | T34012<br>B41035                      | A86518                  | E81564             | T06492 | S17231 | E84809             | S07638 | D70465   | T21428 | S67570             | PSPGA              | PSDG               | T18402             | T43731 | Т39903 | T34510 | T40167 | T16354 | T08538 | в70236 | В97104 | A55423             | C86406 | A96654 | G90594             |
| DNA-directed RNA p<br>hypothetical 527K | 3                  | hypothetical prote chitinase (EC 3.2. | ypop nypothetical prote | conserved hypothet |        |        | hypothetical prote | _      |          |        | hypothetical prote | phospholipase A2 ( | phospholipase A2 ( | asparagine/asparta |        |        |        |        |        |        |        | _      | TpCCT-gamma protei | æ      |        | hypothetical prote |

## ALIGNMENTS

RESULT 1 A42435 A;Molecule type: mRNA
A;Residues: 1-147 <KELL>
A;Cross-references: GB:M81489
A;Cross-references: GB:M81489
A;Note: the authors translated the codon AGC for residue 20 as Arg and GAA for residu A;Note: the authors' translation is shown at residue 65
A;Note: sequence extracted from NCBI backbone (NCBIN:91615) and modified R;Connolly, T.M.; Jacobs, J.W.; Condara, C.
J. Biol. Chem. 267, 6893-6898, 1992
A;Title: An inhibitor of collagen-stimulated platelet activation from the salivary glasses are residues: A42434; MUID:92202246; PMID:1551897 R;Keller, P.M.; Schultz, L.D.; Condra, C.; Karczewski, J.; Connolly, T.M. J. Biol. Chem. 267, 6899-6904, 1992
A;Title: An inhibitor of collagen-stimulated platelet activation from the salivary gl A;Reference number: A42435; MUID:92202247; PMID:1551898
A;Accession: A42435 A;Molecule type: protein
A;Residues: 59-91;101-113;123-139 <CON>
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-147/Product: leech antiplatelet protein #status predicted <MAT> leech antiplatelet protein precursor - Mexican leech C;Species: Haementeria officinalis (Mexican Leech) C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 07-May-1999 C;Accession: A42435; A42434 Best Local Similarity:
Query Match: A; Accession: A42434 Alignment Scores: Pred. No.: Percent Similarity: Score: 0.366 88.50 35.25% 24.59% Length: Matches: Mismatches: Conservative: Indels: 147 30 13 32 47

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US-09-936-737A-1 (1-375) x A42435 (1-147)

1 ATGAAGTATTTCTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCA------

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R:Maggi, L.; Goela, D. submitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid F54D12. A;Reference number: Z21228 A;Accession: T32824
                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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A;Map position: 2
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A; Residues: 1-164 < MAG>
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C; Date: 29-Oct-1999
C; Accession: T32824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F54D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 ArgAsn 120
                                                                                                                                          AAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTAC
  MetAlaTyrSerAsnSerLeuAsn---IleCysTyrLeuTyrAlaValGlyAspValIle
                                                                                                                                                                                                                                                                             PheLeuIleCysTyrValLeuValAsnSerIleMetValSerValArgGlyAlaProGlu
                                                                                                                                                                                                                                                                                                                             TTCTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA
                                              ATCGTTTTTGAAGACACGGTCAACAAGGAATGTTAC---TACAATGTCGTTGATGGTGAA 246
                                                                                            IleAsnSerLeuThrTrpAspGluCysValLysGlnCysLeuSerThrGluIleCysIle
                                                                                                                                                                                                                                    CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCTTTT
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Conservative:
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                                                                                                     hypothetical protein At2g39380 [imported] - Arabidopsis thaliana N,Alternate names: hypothetical protein F12L6.4 C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001 C.Accession: T00548; F84816 C.Accession: T00548; F84816 F8.Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998 A.Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.
A; Molecule type: DNA
A; Residues: 1-637 <R
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C;Superfamily: yeast peptidylprolyl isomerase FPR3; BKBP-type peptidylprolyl isomeras
C;Keywords: nucleus; phosphoprotein
F;324-371/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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A;Title: FKBP46, a novel Sf9 insect cell nuclear immunophilin that forms a protein-ki A;Reference number: A55320; MUID:95074110; PMID:7527037
A;Status: preliminary
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C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 02-Sep-2000
C;Accession: A55320
                                           A; Status: translated from GB/EMBL/DDBJ
                                                                   A; Accession: T00548
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A; Residues: 1-412 <ALN>
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A;Cross-references: EMBL:AC004218; NID:g3355463; PID:g3355467
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounslev, S.D. Shea " D. Donito. . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: tomato leucine zipper-containing protein
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A; Residues: 1-637 <STO>
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A;Map position: 2
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                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                            A; Reference number: Z20343
A; Accession: T27317
                                                                                                                                                                                                      submitted to the EMBL Data Library, August 1997
                                                                A;Cross-references: EMBL:298877; PIDN:CAB11570.1; GSPDB:GN00023; CESP:Y69H2.2
                                                                                            A; Molecule type: DNA
A; Residues: 1-907 <WIL>
                                                                                                                                                                                                                                    R; McMurray, A.
A; Gene: CESP:Y69H2.2
                                          A; Experimental source: clone Y69H2
                        ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 TCTTTACCC------TCGCAGTCTGTCAAATAATTTTCCGTGAAGTTTTCG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 TCAACTTCATCTGACTCGTCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 TCGACAACAAATTTTTCTTGGTCTAACTCTTCACCATCAACGACATTGTAGTAACATTCC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 CATTCGTCAAGA---TCAGAGGACTTC-----TTAAAAGATTTATCGAAGTCTGTA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 TIGITGACCGTGTCTTCAAAAACGATGTAGCAGTACTCCGTCTTGAAACATGTTTTTTIG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SerThrSerSerProLysSerPheLeuSerSerPheProSerPheThrSerLeuProAla 30
                                                                                                                                                                                                                                                                                                                                                                                                                       108 GlnHisLeuMetGlnIleAlaMetAlaArgLeuGlu---LysGluPhePhe 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GluSerIleIleLysLysTrpAspProAsnSerProSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 HispheLeu------IleSerGlnHisSerLysSerAlaLysLeuValLeuAla 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 ---GAGATCAGCAAGCTTGCGAGGCAAAGGAAGGAAATCAAGAAATACTTC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ser---ProLeuAsnGlnThrPheSerGlnSerMetMetGluGluThrValGluAlaAla 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTTTCTGTTCGCGTAAAACGTCCAACAATCTTCACGTTCTTCTGAAGAAGTAGTT--- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisSerArgArgGluAlaLysGluPheIleArgCysIleArgAspLeuArgArgAlaMet 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.00
48.91%
27.74%
12.60%
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A;Map position: 5
A;Introns: 23/3; 65/1; 105/1; 146/1; 191/1; 241/1; 293/1; 381/1; 419/1; 461/1; 499/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.X. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable Athila retroelement ORF1 protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Pate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUID:20083487; PMID:10617197 A,Recession: B84493
                                                                                                                                                                                                                                                                    A;Gene: At2g10660
                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                           A;Cross-references:
                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1303 <STO>
                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                A; Map position:
δõ
                                     US-09-936-737A-1 (1-375) x B84493 (1-1303)
                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                       Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 GluTrpCysMetValSerGluAspMetLeuValLysAspAspValSerMetLysAspAsp 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 ------AAGTCCTCTGATCTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 TyrAlaGlnGluLysSerThrAsp---AspLysThrLeuLysTyrLeuThrLeuCysGly 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 IleGlyThrHisGlnThrLysTyrLysAspAspLysMetThrSerAspLysCysAsnGlu 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 AATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 ValhsnSerArgCysIle-----ValTyrGluAlaGlyGluMetGlu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 TACGCGAACAGAAATATACAGACTTCGATAAATCTTTTAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 ATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 HisGlyMetCysIleAsnTrpGlnSerAspValThrAsp 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 ---ThrAspProAsnAlaCysGluAspAsnSerThrLeuCys---GlyAlaGluLeuGly 311
40 TTGCTGATCTCAACTACTTCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysLysLysSerCysGlyGlyAspSerSerGluTyrCys------GlyLys 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGT 327
                                                                                                                                                                                                                                                                                                              GB:AE002093; NID:94263544; PIDN:AAD15358.1; GSPDB:GN00139
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Matches:
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             --TCAGAAGAACGTGAAGATTGTTGG 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C. submitted to the Protein Sequence Database, May 1996
A;Reference number: S64499
A;Accession: S64507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 7R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
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A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-507 <ARR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane protein YGR189c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G7553
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: S64507
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                                                       367 LysThrLeuAlaSerSerValThrThrSerSerSerIleSerSerPheGluLysGln 386
                                                                                               197 AAAACGATGTAGCAGTACTCCGTCTTG----- 171
                                                                                                                                                                                                             328 ValSerSerSerAlaSerSerThrValSerSerSerValSerSerThrValSerSerSer
                                                                                                                                                                     257 TGGTCTAACTCTTCACCATCAACGACATTGTAGTAACATTCCTTGTTGACCGTGTCTTCA 198
                                                                                                                                                                                                                                               317 TTACCCTCGCAGTCTGTCAAATAATTTTCCGTGAAGTTTTCGTCGACAACAAATTTTTCT 258
                                                                                                                                                                                                                                                                                   308 SerSerSerThrValSerSerSerAlaSerSerThrValSerSerSerValSerSerThr 327
                                                                                                                                                                                                                                                                                                                       371 TCTTCATCAACT-----TCATCTGACTCGTCACCTGTACCTGCGCGCATTACCTGCATCT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 GlnAsnHisGlyGlyTyrAsnLysGlyLysSerIleGlnThrProLysGlu 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 GlyGluThrLeuGlnSerGluLysVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rds: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 ValHisPheLeuGlyAspAspGluThr-------PheGlnValGlnAsp 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 TTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAAACATGT-----TTCAAGACGGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 IleArgThrSerSerAspSerAspGlu-----LysHisCysArgGluMetLysLysHis 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 GluLeuValGluAsnLeuAlaGlnSerAspGlyAsnTyrAsnGluAspTyrGluArgSer 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 MetLeuLeuAspThrThrSerAsnGlyAsnPheLeuAsnLysHisValGluGluGlyTrp 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGD:CRH1; MIPS:YGR189c
                                                                                                                                   SerSerValSerSerSerSerThrSerProSerSerSerThrAlaThr---SerSer 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD:S0003421
                       -- AAACATGTTTTTTTGCATTCGTCAAGATCAGAGGACTTCTTAAAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                               43.18%
31.82%
12.21%
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               RESULT 9
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US-09-936-737A-1 (1-375) \times JC5527 (1-1038)
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
F;1-26/Domain: signal sequence #status predicted <SIG>
F;151-174/Domain: transmembrane #status predicted <TMM>
F;201-508/Domain: protein kinase homology <KIN>
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A;Residues: 1-1038 <BEP>
A;Cross-references: DDBJ;AF003942; NID:92253704; PIDN:AAB63042.1; PID:92253705
C;Comment: This protein is a serine/threonine kinase receptor that forms a heteromeri
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R:Beppu, H.; Minowa, O.; Miyazono, K.; Kawabata, M.

Blochem. Biophys. Res. Commun. 235, 499-504, 1997

A:Title: cDNA cloning and genomic organization of the mouse BMP type II receptor. A:Reference number: JC5527; MUID:97350808; PMID:9207184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone morphogenetic protein type II receptor precursor - mouse C;Species: Mus musculus (house mouse)
121 AspLeuCysAsnValAsnPheThrGluAsnPhe 131
                                                   274 -----GACGAAAACTTCACGGAAAATTAT 297
                                                                                        101 ValThrThrProProSerIleGlnAsnGlyThrTyrArgPheCysCysCysSerThr 120
                                                                                                                                                                                                                                                    211 AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTT 270
                                                                                                                                                                                                                                                                                                                                                        169 TTCAAGACGGAGTACTGCTACATCGTTTTTGAA-------GACACGGTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 LysGlnGlyCysTrpSerHisIleGlyAspProGlnGluCysHisTyrGluGluCysVal 100
                                                                                                                                                                                                                                                                                                       61 SerLysGlySerThrCysTyrGlyLeuTrpGluLysSerLysGlyAspIleAsnLeuVal 80
                                                                                                                                                                                                                                                                                                                                                                                                              41 GlnGlnAspLeuGlyIleGlyGluSerArgIleSerHisGluAsnGlyThrIleLeuCys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 AsnGlnGlu------------ArgLeuCysAlaPheLysAspProTyr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAATATACAGACTTCGATAAATCTTTT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 TTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAAGAAGAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PheArgValProTrpLeuLeuTrpAlaValLeuLeuValSerThrThrAlaAlaSerGln 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 SerSerSerSerLysLysThrValAlaSerSerSerThrSerGluSerIleIleSer 406
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20.61%
11.80%
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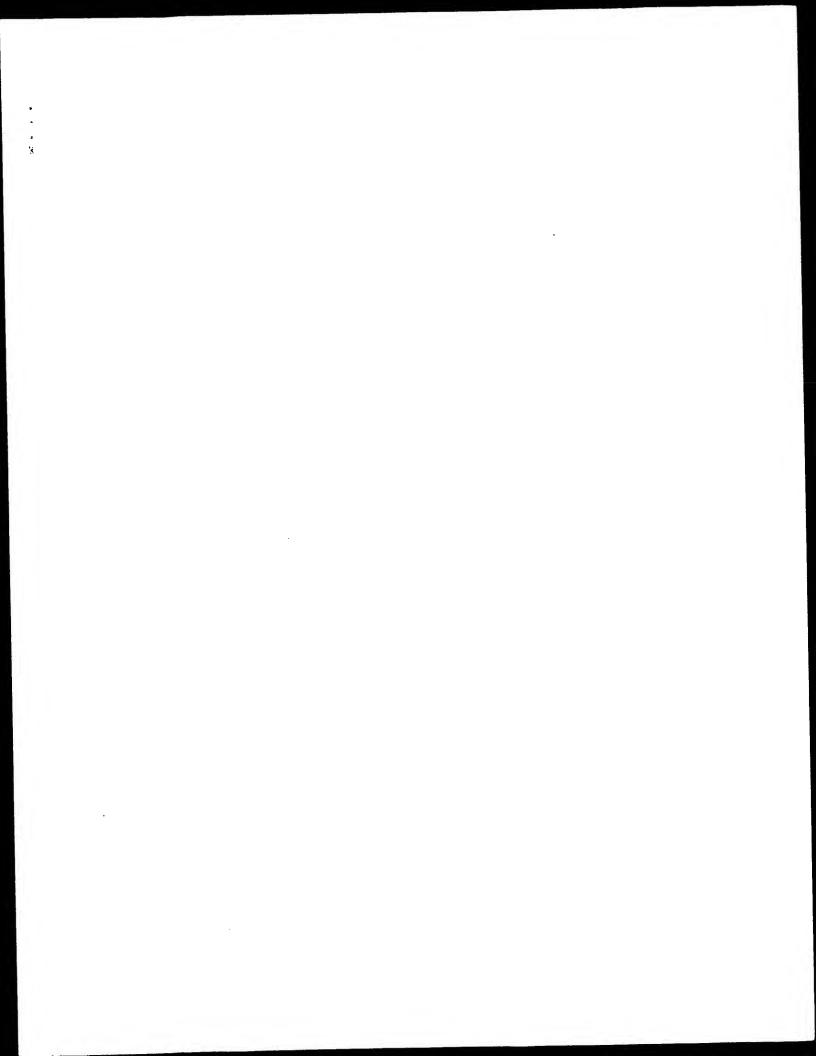
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C;Accession: T32731
R;Comte, P.A.; Ossipow, V.; Schibler, U.
R;Comte, Description: EMBL Data Library, January 1997
submitted to the EMBL Data Library, January 1997
A;Description: Isolation of PIP, a 160 kDa nucleolar protein that interacts with the act A;Description: Isolation of PIP, a 160 kDa nucleolar protein that interacts with the act A;Reference number: Z21213
A;Reference number: T32731
A;Accession: T32731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAR interacting protein - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-1277 <COM>
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                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F40G12.5 - Caenorhabditis elegans c;Species: Caenorhabditis elegans c;Species: Caenorhabditis elegans c;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000 C;Accession: T22054 R.McMurray, A.
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A; Accession: T22054
                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, July 1996
                                                                                                   C; Superfamily: Caenorhabditis elegans hypothetical protein F40G12.4
                                                                                                                                                                                                         A;Cross-references: EMBL:277661; PIDN:CAB01183.1; GSPDB:GN00023; CESP:F40G12.
A;Experimental source: clone F40G12
                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-264 <WIL>
                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                  A; Gene: CESP:F40G12.5
                                                                                                                          A; Introns: 57/3;
                                                                                                                                              A; Map position: 5
                                                             Alignment Scores:
Percent Similarity:
                                             Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    617 LeuGlnLeuIleLeuAlaValLeuAsnProGluThrAsnGluAspGluGluAsp----- 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 AspAlaAspSerAspSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 GATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        658 AspSerLysAsnSerGluSerAspValAspSerGluAspGlyGluGluSerGluGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 GACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 LeuGlnAlaGlyAsnAlaLeuGlyGlyGluGluGluGluGluGlu 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 AAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678 AspArgAspLysAspValAspProGlyPheArgGlnGlnLeuMet------GluVal 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ACGTTTTACGCGAACAGAAATATACAGACTTCGAT---AAATCTTTTAAGAAGTCCTCT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 CTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGT 315
                                                                                                                                   158/3
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40.87%
28.70%
11.80%
    4.31
78.50
41.54%
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                               Matches:
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33
14
43
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26562
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A; Accession: T26562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, September 1999
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A; Residues: 1-550 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone Y26D4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL110478; NID:e1542139; PIDN:CAB54340.1; CESP:Y26D4A.2
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 TTCTTGATTTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AlaProTyrPheGlnLeuGluGluIleGlu 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 GGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 TTCACGGAA-----AATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 TACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTT---GTTGTCGACGAAAAC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 TACATCGTTTTGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 PheAlaIleSerAlaAsnCysSerIleLeuSerPheHisArgAsnLeuLeuGlyGluGlu 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 PheLeuAlaArgAsnLeuIleGlnArgArgGluAlaLeuThrSerGlyLysGluCysPhe 74
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                                                                                                                                                                       170 CysGlyAsnPheLeuHisAsnArgProTyrProAspSerCysGluThrGluCysMetAsp 189
                                             136 TCC---TCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATC 192
                                                                                   190 ThrMetValGlnValAsnAlaLysProGlyProLeuMetGlySerArgAsnIleLysAsp 209
                                                                                                                                                                                                                  79 TGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTC-----
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                                                                                                                                              --GATAAATCTTTTAAGAAG 135
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A;Description: Primary structure
A;Reference number: A36806
A;Accession: A36811
A;Molecule type: DNA
                                                       submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus saimiri genome.
                                                                                                                hypothetical protein ORF48 - saimiriine herpesvirus 1 (strain 11) (Species: saimiriine herpesvirus 1 (strain 11) A; Note: host Saimiri sciureus (common squirrel monkey) (C; Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999 R; Albrecht, J.
                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-936-737A-1 (1-375) x B84021 (1-682)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B84021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-682 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06689.1; GSPDB:GN00A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two-component sensor histidine kinase involved in chemotaxis cheA [imported] - Bacillus C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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                                                                                                                                                                                                                                                                                                                                                                                              213 GluGluLeuGluGluLysPhe-----AspGluArgPheLeuValThrLeuLeuThr 230
                                                                                                                                                                                                                                                                                                                           231 LysValAspGlyGluGlu 236
                                                                                                                                                                                                                                                                                                                                                                      304 GACTGCGAGGGTAAAGAT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GAAGAGTTAGACCAAGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 MetvaipheGluValLeuGluGlnValGly---GluValIleLysSerThrProSerAla 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 ATCGTTTTTGAA-----GACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 GlnIleGluValThrLeuAspGlu-----LysThrLeuLeuLysAlaAlaArgValPhe 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 ------CTTGACGAATGCAAAAAAAACATGTTTCAAGACGGAGTACTGCTAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 TyraspGluPheGluMetThrValLeuAspGlnSerPheGluGlnGlyTyrGlnAlaTyr 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 AsnTyrTyrAspLysAspSerLysGluCysTrpTrpTrpSerIleAspAsnValH1sPhe 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AsnLeuThrSerSerAspGluCysValLysTyrCysTrpLysAspLeuAsnCysPheVal 229
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                                                                       Query Match:
                                                                                        Best Local Similarity:
                                                                                                              Percent Similarity:
                                                                                                                                                                              Alignment Scores:
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A; Introns: 20/3; 124/3
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-191 <WAM>
                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                               A; Gene: CESP: ZC328.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: z18298
A; Accession: T15129
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US-09-936-737A-1 (1-375) x T15129 (1-191)
                                                                                                                                                                                                                                                                C;Superfamily: Caenorhabditis elegans hypothetical protein 2C328.5
                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF000194; NID:g1946990; PID:g1946994; PIDN:AAB52895.1; GSPDB
A;Experimental source: strain Bristol N2; clone ZC328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Wamsley, P.
submitted to the EMBL Data Library, April 1997
A; Description: The sequence of C. elegans cosmid ZC328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZC328.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
C;Accession: T15129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Title: Primary structure of the herpesvirus saimiri ger
A;Reference number: A37309; MUID:92333688; PMID:1321287
A;Contents: annotation; protein-coding frames
A;Note: neither protein nor nucleotide sequence is given
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A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45671.1; PID:g60369
R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;
J. Virol. 66, 5047-5058, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 GluGlyGlu-----AspGluGlyAspGluGlyAspGluGlyAspGlu 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 GCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 GluGlu-----TyrAsnArgAspGluGluGluAspGluGlyGluAspGluGluAspGlu 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 TGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTCAAC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 AlaasnGluLys-----GluTyrLysLysIleIleAspLysSerAspAspArgAspAsp 399
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Search completed: February 25, 2003, 02:29:12 Job time : 27 secs



P53882 saccharomyc P27625 plasmodium

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Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh
-Q=/Cgn2_1/USPTO_spool/US9936737/runat_14022003_100557_1389/app_query.fasta_1.519
-DB=Swissprot_40 -QPMT_fastan -SUFFIX=rsp -MINNATCH+0.1 -LOOPCL=0 -LOOPEXT=0
-DN-Swissprot_40 -QPMT_fastan -SUFFIX=rsp -MINNATCH+0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRAMS=human40.cd1 -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=US0936737_@CGN_1_1_6_@runat_14022003_100557_1389 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-VGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Z222_HUMAN
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MOK1_SCHPO
PA21_CANFA
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ICEC_MOUSE
P2C1_CAEEL
           CHIT_YEAST
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VG48_HSVSA
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Q26486 spodoptera
P53301 saccharomyc
O35607 mus musculu
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Q09337
Q9usk8
P06596
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                           anthocidari
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                                                      Signal.
                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                  SEQUENCE
                                             CHAIN
                                                                          EMBL; M81489; AAA29194.1; -.
                                                                                                                                                                                                                   TISSUE-Salivary gland;
MEDLINE-92202247; PubMed=1551898;
Keller P.M., Schultz L.D., Condra C., Karczewski J., Connolly T.M.;
"An inhibitor of collagen-stimulated platelet activation from the salivary glands of the Haementeria officinalis leech. II. Cloning of the CDNA and expression.";
J. Biol. Chem. 267:6899-6904(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: AN INHIBITOR OF COLLAGEN-STIMULATED PLATELET AGGREGATION, DENSE GRANULE RELEASE AND SEROTONIN RELEASE.
                                                                                                                                                                                                                                                                                                                                                                                            LAPP_HAEOF STANDARD; PKT; 14/ 50. Q01747; Q01747; Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-FEB-1994 (Rel. 28, Last annotation update) 01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                       Haementeria officinalis (Mexican leech).
Bukaryota; Metazoa; Annelida; Clitellata; Hiru
Rhynchobdellida; Glossiphoniidae; Haementeria.
NCBI_TaxID=6410;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 60-91 AND 123-139
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                                                   POTENTIAL.
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MOH1_CANPG
UFE1_YEAST
Y875_METJA
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YCT1_YEAST
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                                                                                                                                                                                                                                                                                                                                                    Clitellata; Hirudinida; Hirudinea;
                          75A5511374A4E42E CRC64;
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P28865 P46995 P49791

rattus norv

homo sapien

rattus norv homo sapien human herpe

escherichia saccharomyc

drosophila methanococc saccharomyc cancer pagu h probable saccharomyc pichia angu saccharomyc mycoplasma homo sapien saccharomyc thermotoga schizosacch

P40157 000507

P81034

P47549 P37265

P04055 Q9x170 P28040

rattus norv

saccharomyc saccharomyc

P34735

0.0379

Length:

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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
46 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans
46 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans
47 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans
48 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans
49 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans
40 kD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95074110; PubMed=7527037;
Alnemri E.S., Fernandes-Alnemri T., Pomerenke K., Robertson N.M.,
Dudley K., Dubois G.C., Litwack G.;
"FKBP46, a novel Sf9 insect cell nuclear immunophilin that forms a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q26486;
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                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 269:30828-30834(1994).

-i- FUNCTION: BINDS TO, AND IS INHIBITED BY FK506 AND RAPAMYCIN. BINDS -i- FUNCTION: BINDS TO, AND IS INHIBITED BY FK506 AND RAPAMYCIN. FOLDING.

DOUBLE-STRANDED DNA IN VITRO. PPIASES ACCELERATE PROTEIN FOLDING.

-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-kinase complex.";
J. Biol. Chem. 269:30828-30834(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TTCGATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAG 174
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7108;
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                                                                                                                                                                                                                         -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 AsnLeuLeuThrLysThrGluPheThrSerValAspGluCysArgLysMetCysGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 ThrileThrAlaGlyAsnGluAspCysTrpSerLysArgProGlyTrpLysLeuProAsp 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ------CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAATATACAGAC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U15038; AAA58962.1; -. HSSP; P20071; 1FKJ.
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                                                                                                                                                                                       p53301;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 52.8 kDa protein in BUB1-HIP1 intergenic region.
YGR189C OR G7553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 AAATATACAGACTTCGATAAATCTTTTAAGAAGTCC-----TCTGATCTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 LeuValProAlaLysAsnLysArgLysLeuGluAsnAlaAsnAspAlaThrAlaAsnLys 135
                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
"DNA sequence analysis of a 23,002 bp DNA fragment of the right arm of Saccharomyces cerevisiae chromosome VII."; yeast 13:357-363(1997).
                                                         Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
                                                                       MEDLINE=97279231; PubMed=9133739;
                                                                                                                                                                                                                                                                                                                                    194 GluGluAspAspAspGluAspGluGluAspGluGluAspAspAsp
                                                                                                                                                                                                                                                                                                                                                                328 AATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGAT 372
                                                                                                                                                                                                                                                                                                                                                                                          177 ---AsnAspGluSerPheLysMetAsn-----ThrSerAlaGluGlyAspAspSerAsp 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 GTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 AspAspAspAsp--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 CTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGA 102
                                                                                        STRAIN-SZUBC
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACG
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                                                                                                                                                                                                                                                                              YEAST
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120
152
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ASP/GLU-RICH (HIGHLY ACIDIC).
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SGD; S0003421; CRH1.
SGD; S0003421; CRH1.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
       O35607;
O35607;
O35607:
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein receptor type II p.
'RMP type II receptor) (BMPR-II) (BRK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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X99074; CAA67525.1; -.
P23904; 1AJK.
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                                                                                                               precursor
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Alignment Scores:
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grant R.A., Begley K.B., Rosenbaum J.S.;
"Identification of BMP receptor complexes with differential signaling properties and ligand binding profiles.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1997) To The EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97350808; PubMed=9207184;
Beppu H., Minowa O., Miyazono K., Kawabata M.;
"CDNA cloning and genomic organization of the mouse BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                            .
No.:
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DOMAIN
                                                                                                                                                                                                                             BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATD; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1. Pfam; PF01064; Activin_recp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein - SUBUNIT: HETERODIMERIZE WITH TYPE-I RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitaker G.B., Koenig B.B.,
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                                                                                                        SEQUENCE
                                                                                                                      CARBOHYD
                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BINDS TO BMP-7, BMP-2 AND, LESS EFFICIENTLY, BMP-4. BINDING IS WEAK BUT ENHANCED BY THE PRESENCE OF TYPE I RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGFB RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOR BMPS
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N-LINKED
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POLY-THR.
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POTENTIAL
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                                                                                                                                                                                                              BY SIMILARITY. POLY-ALA.
                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                          POTENTIAL.
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NKED (GLCNAC. ..) (POTENTIAL)
NKED (GLCNAC. ..) (POTENTIAL)
4106945DC63250E1 CRC64;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                          KINASE.
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Query Match:

Best Local Similarity: Percent Similarity:

Mismatches: Indels:

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Hypothetical gene 48 protein.
  Local Similarity:
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                              EMBL; X64346; CAA45671.1; PIR; A36811; A36811.
                                                                                                                                                                                                                                                                  Albrecht J.-C., Nicholas J., Biller D
Newman C., Wittmann S., Craxton M.A.,
                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
                                     NO.:
                                                                                 Hypothetical
                                                                                                                                                                                                                        "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
-!- SIMILARITY: TO EBV BRRF2.
                                                                                                                                                                                                                                                              Honess R.W.;
                                                                                                                                                                                                                                                                                           MEDLINE=92333688; PubMed=1321287;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Herpesvirus saimiri (strain 11).
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                               VG48_HSVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValThrThrProProSerIleGlnAsnGlyThrTyrArgPheCysCysCysSerThr 120
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                                                                      797 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GACGAAAACTTCACGGAAAATTAT 297
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  2.73
78.00
44.79%
32.29%
                                                                     88867 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                    9E294234AD850E23 CRC64;
            Matches:
Conservative:
Mismatches:
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TCPG_TETPY
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US-09-936-737A-1 (1-375) x VG48_HSVSA (1-797)
                                                    InterPro; IPR002194; Chaperonin_TCP-1.
InterPro; IPR002423; Cpn60/TCP-1.
InterPro; IPR002423; Cpn60/TCP-1.
Pfam; PF00118; cpn60_TCP1; 1.
PRINTS; PR00304; TCOMPLEXTCP1.
PROSITE; PS00750; TCP1_1; FALSE_NEG.
PROSITE; PS00751; TCP1_2; 1.
PROSITE; PS00995; TCP1_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95050756; PubMed=7961900;
Soares H., Penque D., Mouta C., Rodrigues-Pousada C.;
Soares H., Penque D., Mouta C., Rodrigues-Pousada C.;
"A Tetrahymena orthologue of the mouse chaperonin subunit CCT gamma and its coexpression with tubulin during cilla recovery.";
J. Biol. Chem. 269:2929-29307(1994).

-1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON ACTIN AND TUBULIN.

ACTIN AND TUBULIN.
                                      Chaperone;
                                                                                                                                                                                                                                                                                                         EMBL; Z34885; CAA84368.1; -. HSSP; P48425; 1A6D.
                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetrahymena pyriformis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-complex protein 1, gamma subunit (TCP-1-gamma) (CCT-gamma).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER. SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluGlu-----TyrAsnArgAspGluGluGluAspGluGlyGluAspGluGluAspGlu
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ATP-binding; 559 AA; 616
                                                                                                                                                                                                                                                                                                     1A6D.
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61616 MW;
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Alignment Scores:

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RESULT 7
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Best Local Similarity:
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@fisb-sib.ch).
HSSP; P29466; 1ICE
         EMBL; Y13090; CAA73532.1; -.
                                                                                                                              van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
van Loo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
                                                                                                                                                                                                               "Characterization of seven murine caspase family members.";
FEBS Lett. 403:61-69(1997).
                                                                                                                                                                                                                                                                                     MEDLINE=97190206; PubMed=9038361;
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                          Caspase-12 precursor (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICEC_MOUSE
008736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            379 LeuArgGlyAlaSerLysAspValLeuAsnGlu 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 GGTACAGGTGACGAGTCAGATGAAGTTGATGAA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 LysCys-----------GlyLeuPheGluValLysLeuIleGlyAsp 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 ValSerGlyAlaThrIleValAsnArgProGluGluIleGlnGluSerAspValGlyLys 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 CGGAGTACTGCTACATC-----------GTTTTTGAAGACACGGTCAACAAG 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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76.00
42.34%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-936-737A-1 (1-375) x ICEC_MOUSE (1-419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
phosphate.
-!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
                             Taich A., Waterston R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
                                                                                STRAIN-Bristol N2;
                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0376; ILIBGENYME.
SMART; SM00114; CARD; 1
SMART; SM00115; CASC; 1.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS01211; CASPASE_HIS; 1.
PROSITE; PS050208; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                             Probable protein phosphatase 2C F42G9.1 (EC 3.1.3.16) (PP2C).
                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                              P49595;
                                                                                                                                                                                                                                                        P2C1_CAEEL
                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                            346 GACGAG---------TCAGATGAAGTTGAT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                                                                                                                                                                                                                                           295 TATTTG-----ACAGACTGCGAGGGTAAA---GATGCAGGTAATGCGGCAGGTACAGGT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                253 -----GACCAAGAAAATTTGTTGTCGAC-----GAAAACTTCACGGAAAAT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                   82 GluGlnLeuSerLeuGlnPheSerAsnAspGluAspAsp 94
                                                                                                                                                                                                                                                                                                                                                 62 PheLeuGluLysThrAspMetAlaGlyLysIlePheAlaGlyHisIleAlaAsnSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                      42 LeuLysIleGlyGluSerAlaSerPheIleLeuAsnLysAlaGluAsnLeuValGluAsn 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 ValPheAspAspLeuValGluLys------AsnValLeuAsnGlyAspGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; C14.013; -. MGD; MGI:1312922; Casp12. InterPro; IPR001315; CARD. InterPro; IPR002398; ICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thiol protease; Apoptosis; Zymogen.
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.75
75.50
54.79%
35.62%
11.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47853 MW;
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CASPASE-12 SUBUNIT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASPASE-12 SUBUNIT 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B94B0FED16B1CB40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                  491 AA.
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US-09-936-737A-1 (1-375) x P2C1_CAEEL (1-491)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                               RESULT 9
YOFA_CAEEL
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein;
METAL 37 37
METAL 38 38
METAL 57 57
METAL 428 428
METAL 477 477
SEQUENCE 491 AA; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wormpep; F42G9.1; CE07231.
InterPro; IPR001932; PP2C-11ke.
InterPro; IPR000222; PP2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U00051; AAA91358.1; -. HSSP; P35813; 1A6Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00331; PP2C_SIG; 1.
SMART; SM00332; PP2Cc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00481; PP2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                 YOFA_CA
Q09337;
                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 39.7 kDa protein ZKI290.10 in chromosome II precursor.
ZKI290.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 CTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGAC
STRAIN-Bristol N2;
                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                              113 AspIleGlyAspGluGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            205 ACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAA 264
                                               NCBI_TaxID=6239;
                                                                   Rhabditidae;
                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                               101 PheIleArgAlaGlu-----
                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 ValAlaGluCysLeuGlnLysAlaPhe-------ValAspPheAspAsp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 PheThrSerAlaLysLeuProAspPheLeuLysGluArgLysPheTrpGluAlaAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 TACGCGAACAGAAATATACAGACTTC-----GATAAATCTTTTAAGAAGTCCTCTGAT 144
                                                                                                                                                                                                                                                                                                                                                                            TTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCA 324
                                                                                                                                                                                                                                                                                                             GGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                                                                                                                                                                              GlyGlyGluAlaAspSerGluAspGluAlaAspArgIleAsp 137
                                                                                                                                                                                                                  CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS01032; PP2C; 1
                                                                  Peloderinae; Caenorhabditis
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8
75.50
43.62%
24.47%
11.20%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Magnesium; Manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
F110D12E343953D6 CRC64;
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    ------GluSerMetLysGluLeuLys 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
                                                                                                                                                                                                                                                                                                                                                     ----LysProLysLysAla 123
                                                                                                                                                                                                                         360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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FERNANDER RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-936-737A-1 (1-375) x YOFA_CAEEL (1-360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taich A.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00254; ShKT; 1.
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                          Q9UKK8; Q9UKT5; Q9UKK2;
16-QCT-2001 (Rel. 40, Created)
16-QCT-2001 (Rel. 40, Last sequence update)
16-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
Cell wall alpha-1,3-9jucan synthase moki (EC 2.4.1.1)
MOKI OR AGSI OR SPCC338.01C OR SPCC17A7.01.
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomyces pombe (Fission Yeast).
Schizosaccharomyces (Pission Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOK1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 GAAAAATTTGTTGTC-----GACGAAAACTTCACGGAAAATTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 GluAspThrValGlyGluGlu------AsnValPheAspPheAspLysLeuPheAsp 240
                                                                                                                                                                                                                                                                            Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 ThrGluLysThrGlyThrLysLysGlyThrIleGluValSerValGluLeuGlyGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LysLysIleTyrIleArgAsnAspGlySerThrThrGluAsnThrThrGluGlnSerThr 260
MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
                                                                                                                                     and play a role essential for cell morphogenesis and protein kinase function.":
                                                                                                                                                                  SEQUENCE FROM N.A.

Katayama S., Dai H., Arellano M., Perez P., Toda T.;

Katayama S., Dai H., Arellano M., Perez P., Toda T.;

Katayama S., Dai H., Arellano M., Perez P., Toda T.;

Katayama S., Dai H., Arellano M., Perez P., Toda T.;
                                                                                                                                                                                                                                         NCBI_TaxID=4896
                                                                                                                                                                                                                                                                Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 AspAspAspGluGluAsnAspAspAsp 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 GACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                             Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGACTGCGAGGGTAAAGATGCAGGTAAT-------GCGGCAGGTACAGGT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.00
46.38%
33.33%
11.13%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39669 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN ZK1290.10.; 18751B6BC062D4F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2410 AA.
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Qy

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Skelton J. Sjimmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Aert R., Robben J., Grymonprez B.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Eger P., Zimmermann W., Wedler H., Wenther V., Mottler S.M.,
RA Eger P., Zimmermann W., Wedler H., Wenther V., Mottler S.M.,
RA Eger P., Zimmermann W., Wedler H., Wenther E., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wenther S., Mortel B., Warser M., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Egery D., Barrell B.G., Nurse P.;
Shpakovski G., V., Ussery D., Barrell B.G., Nurse P.;
Shpakovski G., V., Ussery D., Barrell B.G., Nurse P.;
RA The genome sequence of Schizosaccharomyces pombe.";
The genome sequence of Schizosaccharomyces pombe.";

"The genome sequence of Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-936-737A-1 (1-375) x MOK1_SCHPO (1-2410)
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InterPro; IPR001296; Glycos_transf_1.
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Cell wall; Transferase; Glycosyltransferase.
CONFLICT 256 F -> Y (IN REF.
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pfam; pr00534; Glycos_transf_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                  650 AspThrHisLeuTrpSerTyrAspCysThrAspGluAspSerAlaIleIleGlyProTrp 669
                                                                                                                                                                                                                                                                                                                                          106 TATACA------GACTTCGATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGC 156
690 SerTrpAsnSerSerTrpGlyCysIleProAsnIle------GluLeuAspPro 705
                                                                                                                                       670 LysSerGlyThrThrLeuArgAsnLeuIleTyrProTyrAspThrIleGluLeuGluAsp 689
                                                                                                                                                                                                      157 AAAAAA-----ACATGTTTCAAGACGGAGTACTGCTAC-----ATCGTTTTTGAAGAC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 ATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAA 105
                                                               205 ACGGTCAACAAGGAA-----TGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
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01-JAN-1988 (Rel. 06, Last sequence update)
01-JUN-1988 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
phospholipase A2 precursor (EC 3.1.1.4) (Phosphopholipase A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 GAAAAATTT------GTTGTCGACGAAAACTTCACGGAAAAT-----TATTTGACA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 GACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGAT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 SerLeuThrProGluHisAspAlaArgValValAlaSerGlyAsnGluIleAsp 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acylhydrolase) (Group IB phospholipase A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohara O., Tamaki M., Nakamura E., Tsuruta Y., Fujii Y., Shin M., Teraoka H., Okamoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Dog and rat pancreatic phospholipases A2: complete amino acid sequences deduced from complementary DNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kerfelec B., Laforge K.S., Vasiloudes P., Puigserver A., Scheele ("Isolation and sequence of the canine pancreatic phospholipase A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=90306027; Pubmed=2142076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kerfelec B., Laforge K.S., Puigserver A., Scheele G.A.; "Primary structures of canine pancreatic lipase and phospholipase A2 messenger RNAS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 190:299-304(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=87175472; pubmed=3562437;
                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way nodified and this statement is not removed. Usage by and for commercial modified requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem.
             pfam; PF00068; phoslip; 1.

PRINTS; PR00389; PHPHLIPASEA2; 1.

PRODOM; PD000303; PhospholipaseA2; 1.

SMART; SM00085; PA2c; 1.

PROSITE; PS00118; PA2_HIS; 1.

PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                             EMBL; D00035; BAA00023.1; ...
EMBL; M35301; AAA30883.1; ...
                                                                                     InterPro: IPR001211; phospholipaseA2.
 Hydrolase; Lipid degradation; Calcium; Pancreas; Signal.
                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                          acylglycerophosphocholine + a fatty acid anion.
COFACTOR: Binds 1 calcium ion per subunit (By similarity).
                                                                                                                                     S11316; S11316.
                                                                                                                                                     A24392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AA
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SIGNAL

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Geus P., van den Bergh C.J., Kuipers O., Verheij H.M.,
Hoekstra W.P.M., de Haas G.H.;
"Expression of porcine pancreatic phospholipase A2. Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                     MEDLINE=87231066; PubMed=3295782;
                                                                             TISSUE=Pancreas;
                                                                                      SEQUENCE FROM N.A.
                                                                                                          Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                            21-70L-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 05, Last sequence update)
15-70N-2002 (Rel. 41, Last annotation update)
Phospholipase A2, major isoenzyme precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IB phospholipase A2).
                                                                                                                                                                                                                                                                PA21_PIG
P00592;
                                                                                                                                                                                                                                                                                                                              262 AAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGAT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                59 ProvalAspGluLeuAspLysCysCysGlnThrHisAspHisCysTyr-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 AspProLeuLysAspTyrAsnAspTyrGlyCysTyrCysGlyLeuGlyGlySerGlyThr 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 IleSerProArgAlavalTrpGlnPheArgAsnMetIleLysCysThrIleProGluSer 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 -----CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACA------ 111
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                                                                                                                                                                                                                                                                                                                                                                                    GACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTICGATAAATCTTTTAAG------141
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38.33%
24.17%
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BY SIMILARITY
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VIA CARBONYL OXYGEN (BY SIMILARITY).

VIA CARBONYL OXYGEN (BY SIMILARITY).

VIA CARBONYL OXYGEN (BY SIMILARITY).

VIA CARBONYL OXYGEN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                           ...-SerGluAlaLysLysLeuAspSerCys 83
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Indels:
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AC OC OC OC RP RP RA RX RA RA RA

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STROCTURE BY NMR.

STROCTURE BY NMR.

MEDLINE=95393214; PubMed=7664098;

van den Berg B., Tessari M., Boelens R., Dijkman R., de Haas G.H.,

Kaptein R., Verheij H.M.,

"NMR structures of phospholipase A2 reveal conformational changes
                                                                                              "Porcine pancreatic phospholipase A2: sequence-specific 1H and 15N MMR assignments and secondary structure."; Biochemistry 30:3135-3147(1991).
                                                                                                                                                          Dekker N., Peters A.R., Slotboom A.J., Boelens R., Kaptein R.,
                                                                                                                                                                                                           STRUCTURE BY NMR.
                                                                                                                                                                                                                  Thunnissen M.M.G.M., Kalk K.H., Drenth J., Dijkstra B.W.;
"Structure of an engineered porcine phospholipase A2 with enhanced activity at 2.1-A resolution. Comparison with the wild-type porcine and Crotalus atrox phospholipase A2.";
J. Mol. Biol. 216:425-433(1990).
                                                                                                                                                                                                MEDLINE=91175768;
                                                                                                                                                                                                                                                                                                                                                 Dijkstra B.W., Renetseder R., Kalk K.H., Hol W.G.J., Drenth J., "Structure of porcine pancreatic phospholipase A2 at 2.6-A resolution and comparison with bovine phospholipase A2.",
                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=91073405; PubMed=2254938;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-8925548B. PubMed=2498336;
Tomasselli A.G., Hui J., Fisher J., Zuercher-Neely H., Reardon H.M., Oriaku E., Kezdy F.J., Heinrikson R.L.;
"Dimerization and activation of porcine pancreatic phospholipase A2 y.Biol. Chem. 264:10041-10047(1989).
                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS), AND ACTIVE AND BINDING SITES.
MEDLINE-83268704; PubMed-6876174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Haas G.H., Slotboom A.J., Bonsen P.P.M., Nieuwenhuizen W., van Deenen L.L.M., Maroux S., Dlouha V., Desnuelle P., "Studies on phospholipase A and its zymogen from porcine pancreas. II. The assignment of the position of the six disulfide bridges.", Biochim. Biophys. Acta 221:54-61(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACYLATION OF LYS-78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Puljk W.C., Verheij H.M., de Haas G.H.;
"The primary structure of phospholipase A2 from porcine pancreas.
reinvestigation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sellhamer J.J., Randall T.L., Yamanaka M., Johnson L.K.; "Pancreatic phospholipase A2: isolation of the human gene and cDNAs from porcine pancreas and human lung.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=71014235; PubMed=5528841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          active enzyme by sequence-specific cleavage Escherichia coli.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 15:3743-3759(1987).
                                                                                                                                                                                        PubMed=2007145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Haas G.H., Verheij H.M.;

de Haas G.H., Verheij H.M.;

"Solution structure of porcine pancreatic phospholipase A2 complexed with micelles and a competitive inhibitor.";

J. Biomol. NMR 5:110-121(1995).

-I. FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.

-I. CATALYTIC ACTIVITY: Phosphatidylonline + H(2)0 = 1-
                               DISULFID
                                              DISULFID
                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                            ProDom; PD00030; SMART; SM00085;
                                                                                                                                                                                                                                                                                                                      InterPro; IPR001211; PhospholipaseA2
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
                                                                                                                                                                                                                                                                  PROSITE; PS00118; PA2_HIS; 1. PROSITE; PS00119; PA2_ASP; 1.
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                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                     Hydrolase;
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MEDLINE=96016184; PubMed=7556053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acylglycerophosphocholine + a fatty acid anion.
COFACTOR: Binds 1 calcium ion per subunit.
SUBUNIT: MONOMER OR HOMODIMER.
SUBCELLULAR LOCATION: Secreted.
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15-OCT-94.
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15-JUL-93.
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                                                                                                                                       ACTIVATION PEPTIDE.

PHOSPHOLIPASE A2, MAJOR ISOENZYME.

PYRROLIDONE CARBOXYLIC ACID.

ACTIVITY LOST UPON ALKYLATION WITH

P-BROMO PHENACYL BROMIDE; CA++, BA++

PROTECT AGAINST INACTIVATION.
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  VIA CARBONYL OXYGEN
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(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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InterPro; IPR000822; Znf_C2H2.
InterPro; IPR000862; Znf_C2H2.
Pfam; PF001352; KRAB; 1.
ProDom; PD001003; Znf_C2H2; 5.
SMART; SM00349; KRAB; 1.
SMART; SM00355; Znf_C2H2; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Differential expansion of homologous zinc-finger gene families human chromosome 19413.2 and mouse chromosome 7."; Submitted (SEP-199) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MAX FUNCTION AS A TRANSCRIPTION FACTOR.
-i- SUBCELLULAR LOCATION: Nuclear (Probable).
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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CysAspGluCysGlyLysSerPheCysTyrIleSerAlaLeuHisIleHisGlnArgVal 166
                                                        CTTGACGAATGCAAAAAAACA-----
                                                                                                            SerAspValSerPhePheAspLeuProGlnGlnLeuTyrSerGlyGluLysSerHisThr 146
                                                                                                                                                                  GCGAACAGAAATATACAGACTTCGATAAA-----
                                                                                                                                                                                                                     LeuSerThrValHisThrArgGluLysProPheGlnGlyGluAsnCysLysGlnPhePhe 126
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                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                Hypothetical protein; Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein AQ_1923 precursor
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000763; AAC07719.1;
                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=63363;
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 AspLysThrLeuArgLysSerGly----
                               TyrPheAlaTyrAspLysTyrMetAspAsnLysAlaLysGluGlnValGluTyrPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ysGlyLysGlyPheArgCysArgSerAlaLeuLysValHisCysLysLeuHisMetArgG
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                                                                                             TTTTACGCGAACAGAAAATATACAGAC-----
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                                                                                                                                                                                                                                                                                      296 AA;
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(Rel. 40, Last sequence up
(Rel. 40, Last annotation
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                                                                                                                                                                                                                                                                                      HYPOTHETICAL PROTEIN AQ_1923; 9C88F4456AA9449C CRC64;
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OC CURATY
OX MEDLIN
RR FOSDAU
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DR GLYCOS
DR DLICTD
DR SMARR;
DR GLYCOS

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                                                                                                                                                                   US-09-936-737A-1 (1-375) x SP96_DICDI (1-600)
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                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fosnaugh K., Loomis W.F.;
"Sequence of the Dictyostellum discoideum spore coat gene SP96.";
Nucleic Acids Res. 17:9489-9489(1989).
-1- SUBCELLULAR LOCATION: OUTER LAYER OF THE COAT MATRIX AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlycoSuiteDB; P14328; -.
DictyDb; DD03007; cotA.
InterPro; IPR003645; FolN.
SMART; SM00274; FOLN; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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  311 TCGCAGTCTGTCAAATAATTTTCCGTGAAGTTTTCGTCGACAACAAATTTTTCCTTGGTCT 252
                                                       488 SerSerSerAlaSerSerSerSerSerProSerSerSerAlaSerSerSerSerAlaPro 507
                                                                                                         371 TCTTCATCAACTTCATCTGACTCGTCACCTGTACCTGCCGCATTACCTGCATCTTTACCC 312
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PRESPORE MOTIF 4.
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Search completed: February 25, 2003, 02:26:31 Job time : 16.5 secs

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-Q-/cgn2_1/USPF0_spool//US0936737/runat_14022003_100557_1398/app_guery.fasta_1.519
-DB-SPTREMBL_21 -QPMT-fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=-human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-DOCALIGN=200 -THR_SCORE=PCt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0.000000000
-UNITS=0-NORM=-CCN 1_1_34_@runat_14022003_100557_1398 -NCPU=6 -TCPU=3
-UNITS=0-NORMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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-MODEL=frame+_n2p.model -DEV=xlh
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                                                                                                                                                  pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_mammal:*
                                                                                                                                                                                                                                                                                                sp_unclassified:*
sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                             sp_vertebrate:*
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                                                                                                                                                                                                                                                                         sp_bacteriap:*
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5 097239
                                                                                                                 SUMMARIES
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7.0
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                                                     Description
     097239 plasmodium
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| 38<br>44<br>42<br>44<br>44<br>44<br>44   | 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                              | 2000<br>2000<br>2000<br>2000<br>2000<br>2000<br>2000<br>200  | 10<br>11<br>12<br>13<br>14<br>15<br>16<br>17  | <b>3ω4υδρω</b>   |
|--|--|--|---|--|
| 74.5<br>74.5<br>74.5<br>74.5<br>74.5<br>74.5   |  | 76.5<br>76.5<br>76.5<br>76.5<br>76.5<br>75.5<br>75.5   | 79.5<br>79.5<br>78.5<br>78.5<br>78.5<br>78.5  | 444  |
| 11.4<br>11.4<br>11.1<br>11.1<br>11.1<br>11.1<br>11.0                                   | 11.5   | 111.4<br>111.4<br>111.4<br>111.3<br>111.3<br>111.3   |   | 12.5<br>12.2<br>12.2<br>12.2<br>12.6<br>12.6<br>12.6                         |
| 328<br>451<br>469<br>606<br>643<br>248   | 324<br>324<br>534<br>782<br>782<br>2410<br>3844                    | 945<br>168<br>143<br>786<br>1255<br>1278<br>336<br>336<br>703<br>719   | 1277<br>1277<br>1358<br>116<br>264<br>509<br>550<br>682<br>191<br>191<br>1257   | 164<br>368<br>374<br>374<br>637<br>907<br>388                                |
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| Q12140<br>Q12140<br>Q9P1U5<br>Q8VMW8<br>Q9FIW8<br>Q9FIW8<br>Q9XV53<br>Q9XV79<br>Q65239 | Q950M3 P87179 O94317 Q91KR5 P78852 Q94648 Q85554                   | Q03650<br>Q01Q13<br>Q9LQ13<br>Q8W9Z1<br>Q9C7E7<br>Q9C7I16<br>Q50667<br>Q9SZQ0<br>Q9TIR7<br>Q9SZQ0<br>Q9TIR7<br>Q9LKR9<br>Q9263 | 035821<br>085RA3<br>08XJ41<br>020246<br>020246<br>09V9S1<br>09W204<br>09K8N5<br>09K8N5  | )44835<br>29VFH8<br>29VFH8<br>080625<br>080783<br>098783<br>098830           |
| saccharchomo san<br>listeria<br>arabido<br>caenorho<br>drosoph<br>g african            | tap<br>chi<br>chi<br>ara<br>ara<br>chi<br>chi<br>las<br>ros<br>mus | 50 ti<br>q13 i<br>q13 i<br>7e7 di<br>7i16<br>7i16<br>7i16<br>7i16<br>7i16<br>7i16<br>7i16<br>7i1                               | 035821 rattus norv 08sra3 encephalito 08s/41 clostridium 020246 caenorhabdi 09x9s1 streptococc 09u244 caenorhabdi 09k8n5 bacillus ha 002052 caenorhabdi 09n57 caenorhabdi 098pq6 mycoplasma | enorha<br>osophi<br>osophi<br>osophi<br>rabido<br>enorha<br>hermoa<br>rabido |

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## ALIGNMENTS

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097239;
                                    Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., Gentles S., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.; Whitehead S., Woodward J.R., Newbold C., Barrell B.G.; The complete nucleotide sequence of chromosome 3 of Plasmodium falls.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 467-9 kDa protein.
PEC0245C, MAL3P2.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99376085; PubMed=10448855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-3D7
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falciparum .";
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                      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Charles B., Charles B
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                          MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 044835
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PROSITE; PS00018; EF_HAND; UNKNOWN_1.
Hypothetical protein.
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EMBL; AL034558; CAB39005.1; -.
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             J., Percy C., Rifken L., Roopra A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peloderinae; Caenorhabditis.
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45.52%
24.83%
13.28%
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 AA.
Saunders D., Shownkeen R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3933
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Q9VFHB
AC QS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                                                                           Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG14853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG14853 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VFH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9VFH8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 GAGTTAGACCAAGAAAAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 ATCGTTTTTGAAGACACGGTCAACAAGGAATGTTAC---TACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AAGAAGTCCTCTGATCTTGACGAATGCAAAAAAAACATGTTTCAAGACGGAGTACTGCTAC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
Submitted (DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of C. elegans cosmid F54D12.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 MetalaTyrSerAsnSerLeuAsn---IleCysTyrLeuTyrAlaValGlyAspValIle 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 IleAsnSerLeuThrTrpAspGluCysValLysGlnCysLeuSerThrGluIleCysIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 CGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCTTTT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 IleSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PheLeuIleCysTyrValLeuValAsnSerIleMetValSerValArgGlyAlaProGlu 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluValArgHisAspGln 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tted (DEC-1997)
AF040647; AAB94
                                                                                                                                                                                                                                                                                                                                                              Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 AA; 19130 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                  Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1997) to the EMBL/GenBank/DDBJ databases AAB94992.1; -.
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26.74%
12.54%
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84.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D3C070A63C493716 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Baros P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Durbin K.J., Evangelista C.C., Ferriara S., Fleischmann W., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Towland T.J., Wall M.-H., Deywam C., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lusk C., Mattei B., McIntosh T.C., McIeod M.P., McPherson D., RA Lusk C., Pittman G.S., Pan S., Poller J.M., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G., RA Rainert K., Remington K.A., Singers R.D.C., Scheeler F., Spendling A.C., Stapleton M., Skupski M.P., Smith T., RA Rainers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Rainers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Rainers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Rainers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Rainers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Rainers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Rainers E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Rainers E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Rainers E., Spradling A.C., Stapleton M., Stupski M.P., Smith T., Rainers E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O., Rainers E., Spradling A.C., Stapleton M., Stupski M.P., Zhu X., Smith H.O., Rainers E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.
313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity:
                                              159 AsnTyrAsnLysSerSerSerProAspLeuAlaLeuAspLeuHisAlaSerAspValGlu 178
                                                                                                                                                                                                                                          123 CysLysLeuIleLeuGlnTyrGluProAspAsnAlaThrAlaLysGluPheTyrProLeu 142
                                                                                                                                                                                                                                                                                            184 TGCTACATCGTTTTTGAA------GACACGGTCAACAAGGAATGTTACTACAATGTC 234
                                                                                                               280 AACTTCACGGAAAAT-----
                                                                                                                                                                                            106 GluPheLeuSerAlaValMetLeuLysAspTyrLysLysAla------LeuLysTyr 122
                                                                                                                                                                                                                                                                                                                                                                                      127 ---TITAAGAAGTCCTCTGATCTTGACGAATGCAAAAAACATGTTTCAAGACGGAGTAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTAC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GluTyrThrAspAlaAspGluSerValSerAlaProThrGluPheLeuAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGAACAGAAAATATACAGACTTCGATAAATCT------ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaSerGlyLeuProThrSerAlaSerSerGluAspLeuSerGlnSerLeuSer----- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 AA;
                                                                                                                                                -----LeuAspLysLeuArgAlaValAlaThrSerSerAspSerAspGlu
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82.50
42.14%
24.29%
12.24%
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Conservative:
Mismatches:
Indels:
                                                                                                  --TATTTGACAGACTGCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
                                      080625;
                                                      080625
                                                                                                  185 AlaAspValAspGlyAspGluAlaGlyAspAlaAspGluAspGlyAspAlaAspAlaAsp 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                        149 Ile-----LeuAspLysLeuArgAlaValAlaThrSerSerAspSerAspGlu 164
                                                                                                                                                                                                   280 AACTTCACGGAAAAT-----
                                                                                                                                                                                                                                                   129 CysLysLeuIleLeuGlnTyrGluProAspAsnAlaThrAlaLysGluPheTyrProLeu 148
                                                                                                                                                                                                                                                                                                              184 TGCTACATCGTTTTTGAA------GACACGGTCAACAAGGAATGTTACTACAATGTC 234
                                                                                                                                                                                                                                                                                                                                          112 GluPheLeuSerAlaValMetLeuLysAspTyrLysLysAla------LeuLysTyr 128
                                                                                                                                                                                                                                                                                                                                                                       127 ---TTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RE63320p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8SYG5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8SYG5
                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GCGAACAGAAATATACAGACTTCGATAAATCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 AlaSerGlyLeuProThrSerAlaSerSerGluAspLeuSerGlnSerLeuSer----- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTAC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AlaAspValAspGlyAspGluAlaGlyAspAlaAspGluAspGlyAspAlaAspAlaAsp 198
                                                                                                                                GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                             AsnTyrAsnLysSerSerSerProAspLeuAlaLeuAspLeuHisAlaSerAspValGlu 184
                                                                                                                                                                                                                                                                                                                                                                                                     ------GluTyrThrAspAlaAspGluSerValSerAlaProThrGluPheLeuAla 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY071572; AAI
NCE 374 AA;
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL49194.1;
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42.148
24.298
12.248
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                                               PRT;
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Indels:
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                                                 637
                                                                                                                                                                                             -----TATTTGACAGACTGCGAG 312
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Alignment Scores: Pred. No.:
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                               RESULT 6
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            Q9XTS9
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AT2G39380.
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bownan C.L., Barnstead M.E., Feldblyum T.V.,
Fujii C.Y., Mason T.M., Bownan C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.,
Salzberg and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Last annotation update) At2g39380 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004140; Exo70. Pfam; PF03081; Exo70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; ACC004218; AAC27829.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA;
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Q9XTS9
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                                                                    108
                                                                                                                                                                     107 TATTTTCTGTTCGCGTAAAACGTCCAACAATCTTCACGTTCTTCTGAAGAAGTAGTT---
                                                                                                                                                                                                                                               155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SerThrSerSerProLysSerPheLeuSerSerPheProSerPheThrSerLeuProAla 30
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                                                                                                                                                                                                                                           CATTCGTCAAGA---TCAGAGGACTTC-----TTAAAAGATTTATCGAAGTCTGTA 108
                                                                                                                                                                                                                                                                                                                                                                                  TCGACAACAATTTTTCTTGGTCTAACTCTTCACCATCAACGACATTGTAGTAACATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTTACCC-----TCGCAGTCTGTCAAATAATTTTCCGTGAAGTTTTCG 276
                                                                                                                                                                                                                                                                                                                 TTGTTGACCGTGTCTTCAAAAACGATGTAGCAGTACTCCGTCTTGAAACATGTTTTTTTG 156
                                                                                                                                                                                                                                                                                                                                                 GluSerIleIleLysLysTrpAspProAsnSerProSer---------
                                                                  GlnHisLeuMetGlnIleAlaMetAlaArgLeuGlu---LysGluPhePhe 123
                                                                                                 ---GAGATCAGCAAGCTTGCGAGGCAAAGGAAGGAAATCAAGAAATACTTC 3
                                                                                                                                      HisPheLeu------IleSerGlnHisSerLysSerAlaLysLeuValLeuAla
                                                                                                                                                                                                        {\tt HisSerArgArgGluAlaLysGluPheIleArgCysIleArgAspLeuArgArgAlaMet}
                                                                                                                                                                                                                                                                                                                                                                                                                     Ser---ProLeuAsnGlnThrPheSerGlnSerMetMetGluGluThrValGluAlaAla
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 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.61
82.00
48.91%
27.74%
12.60%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72179 MW;
                                                                                                                                                                                                                                                                                  -----TyrThrLysIleIleSerLeuPheSer
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     PRT;
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Conservative:
Mismatches:
     907
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Pfam; PF00008; EGE; 7.
PRINTS; PR01078; AMINACHANNEL.
PRINTS; PR01078; EGFBLOOD.
SMART; SM00181; EGF; 8.
SMART; SM00181; EGF; 8.
PROSITE; PS01186; EGF_1; UNKNOWN.
PROSITE; PS01186; EGF_2; 4.
EGF-like domain; Glycoprotein.
SEQUENCE 907 AA; 101840 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XTS9;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 282:2012-2018(1998).
EMBL; 298877; CAB11570.1; -.
HSSP; Q12784; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000561; EGF-like.
InterPro; IPR001438; EGF_II.
InterPro; IPR001873; Na+channe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Investigating biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match:
                                                                                                                                                                                                                                       245 GluTrpCysMetValSerGluAspMetLeuValLysAspAspValSerMetLysAspAsp 264
                                                                                                                                                                                                                                                                                                 226 TyrAlaGlnGluLysSerThrAsp---AspLysThrLeuLysTyrLeuThrLeuCysGly 244
                                                                                                                                                                                                                                                                                                                                                             206 IleGlyThrHisGlnThrLysTyrLysAspAspLysMetThrSerAspLysCysAsnGlu
                                                                                                                                                                                                           154 TGCAAAAAAACATGT-----TTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACG 207
312 HisGlyMetCysIleAsnTrpGlnSerAspValThrAsp
                             328 AATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                    280 ValAsnSerArgCysIle-----ValTyrGluAlaGlyGluMetGlu-----
                                                                                                                                                                                                                                                                                                                                                                                          46 ATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTT-----
                                                                                                                                                                                                                                                                                                                                 91 TACGCGAACAGAAAATATACAGACTTCGATAAATCTTTTAAG------
                                                                                        GTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGT 327
                                                                                                                                                GTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTT 267
                                                                                                                                                                             CysLysLysSerCysGlyGlyAspSerSerGluTyrCys-------GlyLys 279
                                                                                                                                                                                                                                                                          -----AAGTCCTCTGATCTT-----
                                                          ---ThraspProAsnAlaCysGluAspAsnSerThrLeuCys---GlyAlaGluLeuGly 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF_1; UNKNOWN_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.00
39.85%
27.82%
12.17%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8B55FF139F8F81D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
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37
16
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Q9SKSO
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                       Putative Athila retroelement ORF1 protein.
                                                                                                                                                Q9SKSO;
                                                                                                                                                                  Q9SKS0
                                                                                                                                                                                                                                    289 GAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAAT 330
                                                                                                                                                                                                                                                                                        229 AATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGACGAAAACTTCACG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21992816; PubMed-11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Ya Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Tai X., Huang L., Dong X., Ma Y., Ya Tan H., Chen R., Wang J., Yu J., Yang H.;
Genome Res. 12:689-700(2002).
EMBL; AE013191; AAM25634.1;
Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                  181 TACTGCTACATCGTT-----TTTGAAGACACGGTC-----AACAAGGAATGTTACTAC 228
                                                                                                                                                                                                       88 LysAsnAlaLeuIleGlyThrIleAspLysAspGlySerAsn 101
                                                                                                                                                                                                                                                            68 ArgLeuProIleLysLeuAsnLeuGlyIleGluSerPheIleLeuThrSerProSerGly 87
                                                                                                                                                                                                                                                                                                                                                                                                           121 AAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAG 180
                                                                                                                                                                                                                                                                                                                                                                               32 TyrGlnPheAsnLysSerSerAsp------ProLysLeuValTyrAlaAspGlu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MB4T / JCM11007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein TTE2505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MetArgTyrPheLeuLeuAlaValLouMetValAlaSerLeuIleLeuValSerCysSer 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGAAGTATTTCTTGATTTCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8R7B3;
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                                                                                                                                                                                                                                                                                                                       AsnLysVallieIleAsnAspGlyGluAspMetValValGluSerArgGlyAsnPheTyr 67
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Complete proteome.
88 AA; 44282 MW; 39FAB7E1291E8AlF CRC64;
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28.95%
12.02%
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81.00
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                                                                                                                                                   PRT;
                                                                                                                                                 1303 AA
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Indels:
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S S D D D AC
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
                                                                      Q94BY9;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                            AT5g53570/MNC6_11
                                                                                                                                             Q94BY9
                                                                                                                                                                                    250 GlnAsnHisGlyGlyTyrAsnLysGlyLysSerIleGlnThrProLysGlu 266
                                                                                                                                                                                                                    301 ACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAG 351
                                                                                                                                                                                                                                               238 GlyGluThrLeuGlnSerGluLysVal------AsnTyrVal
                                                                                                                                                                                                                                                                              241 GGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTG 300
                                                                                                                                                                                                                                                                                                                                          181 TACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGAT 240
                                                                                                                                                                                                                                                                                                            224 ValHisPheLeuGlyAspAspGluThr-------PheGlnValGlnAsp 237
                                                                                                                                                                                                                                                                                                                                                                       206 IleArgThrSerSerAspSerAspGlu-----LysHisCysArgGluMetLysLysHis 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. IRMBL; AC006250; AAD15358.1; -
InterPro: IPR004312; ATHILA.
InterPro: IPR001230; Prenyl_site.
Pfam; PF03078; ATHILA; II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA;

MEDLINE=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                      127 TTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAAACATGT-----TTGAAGACGGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                  186 GluLeuValGluAsnLeuAlaGlnSerAspGlyAsnTyrAsnGluAspTyrGluArgSer 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 MetLeuLeuAspThrThrSerAsnGlyAsnPheLeuAsnLysHisValGluGluGlyTrp 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00294; PRENYLATION; UNKNOWN 1.
SEQUENCE 1303 AA; 148843 MW; 1113D37B999C303E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 TIGCTGATCTCAACTACTTCT-----TCAGAAGAACGTGAAGATTGTTGG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. COLUMBIA;
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                                                                                                                                       PRELIMINARY;
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80.50
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                                                              Last annotation update)
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                                                                                 sequence update)
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Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Miranda M., Narusaka M., Nguyen M., Satou M., Seki M., Southwick A.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis CDNA clones.";
"Arabidopsis CDNA clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 TOGCAGTOTGTCAAATAATTTTCCGTGAAGTTTTCGTCGACAACAATTTTTCTTGGTCT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 -----
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                                                                             01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 SerSerGlyAsnSerSerSerSerSerSerLeuProSerSerSerSerSerSerLeuPro
                                                                                                                                                                                                                                                                                                                                       110 LysLeuArgAspGlyGlyValGlyPheLeuLysLysValArgSerArgGlyValAspPro 129
                                                                                                                                                                                                                                                                                                                                                                      146 AGATCAGAGGAC-----TTCTTAAAAGATTTATCG------117
                                                                                                                                                                                                                                                                                                                                                                                                                                      194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 SerSerSerSerSer-----SerProProSerSerAsnSerAsnSerTyrSerAsnSer 49
                                                 PAR interacting protein. Rattus norvegicus (Rat).
                                                                                                                                 035821;
                                                                                                                                                  035821
                                                                                                                                                                                                                                                                         130 SerIleArgAlaGluValTrpLeuPheLeuLeuGlyValTyrAspLeuAsnSerThrSer 149
   NCBI_TaxID=10116;
                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                             150 GluGluArgGluAlaValLys-----ThrGlnLysArgLysGluTyrGluLys 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                   90 ArgLysArgLysTrpAlaLeuThrProHisGlnTrpArgSerLeuPheThrProGluGly 109
                                                                                                                                                                                                                                          62 GAAGAAGTAGTTGAGATCAGCAAGCTTGCGAGGCAAAGGAAAGGAAATCAAGAAA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuSerSerProSerSerValThrSerSerAspArgArgArgLysSerProTrpSerArg 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnSerSerSerSerSerSerTrpIleHisLeuArgSerValLeuPheValAlaAsn 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AAGTCTGTATATTTTCTGTTCGCGTAAAACGTCCAACAATCTTCACGTTCTTCT 63
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                                  Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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US-09-936-737A-1 (1-375) x 035821 (1-1277)
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"Isolation of PIP, a 160 kDa nucleolar protein that interacts with
activation domain of PAR transcription factors.";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U83590; AAB62878.1;__.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91084854; PubMed=2261643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617 LeuGlnLeuIleLeuAlaValLeuAsnProGluThrAsnGluAspGluGluAsp-----
                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Type II protein farnesyltransferase beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 ------AsnvalvalvalrhrAspThrAspGluLysGlnLeuLysHisGlyGlu 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 AspalaAspSerAspSer------Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 GACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 CTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGG 84
                                                                                                                                                                                          Encephalitozoon cuniculi.
                                                                                                                                                                                                                                                                                               Q8SRA3
                                                                                                                                                                                                                                                                                                                                                                                316 AAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                           678 AspargAspLysAspValAspProGlyPheArgGlnGlnLeuMet------GluVal 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 ACGTTTTACGCGAACAGAAATATACAGACTTCGAT---AAATCTTTTAAGAAGTCCTCT 141
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
                                                                                                                                                                         Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                                                                  695 LeuGlnálaGlýásnálaLeuGlýGlyGluGluGluGluGluGlu
                                                                                                                       STRAIN-GB-M1;
                             MEDLINE=21576510; PubMed=11719806;
                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=6035;
                                             STRAIN=GB-M1;
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspSerLysAsnSerGluSerAspValAspSerGluAspGlyGluGluSerGluGluGlu 677
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90; AAB62878.1; -.
1277 AA; 144675 MW; 43140A2973178792 CRC64;
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Alignment Scores:
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            flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003192; BAB81626.1;
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 3.
SMART; SM00028; TPR; 3.
Hypothetical protein; Complete proteome.
SEQUENCE 116 AA; 13590 MW; 9D6B5D847B3A7312 CRC64;
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Score: 79.00
Percent Similarity: 41.748
Best Local Similarity: 24.358
Query Match: 11.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores: Pred. No.:
                                                                                                                                   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                    QBXJ41;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein CPE1920.
                                                                                                                                                                                                                                              Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1502;
                                                                                                                                                                                                       PubMed=11792842;
                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-13 / TYPE A
                                                                                                                                                                                                                                                                                                                                                                                                                Q8XJ41
                                                                                                                                                                                                                                                                                                                                                                                                                                               316 GlyproserGlyGlypheSerAspArgProGlyAsnGluThrAsp 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGAT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 GAAGACACGGTC-----AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 ThrArg-----PheIlePheSerCysGln 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 SerSerLeuValLeuIleGlyLysGluCysTyr-----ValAsnGlnGluGluLeu 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 LysLysGluAspValCys-----290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 TCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 valalaArgPheIleAlaThrLysGlnAlaSerSerGlyGlyLeuSerGlyArgValSer 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 PheCysCysLeuSerThrLeuArgSerLeuGlyAlaLeuGluThrValAspArgGluGlu 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
Nature 414:450-453(2001).
EMBL; AL590448; CAD26435.1;
SEQUENCE 358 AA; 40074 MW; CCABFD0245F98342 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 TGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCTTTTAAGAAGTCC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TTCCTTTGCCTCGCAAGCTTG---CTGATCTCAACTACTTCTTCAGAAGAACGTGAAGAT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                  TYPE A;
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
8.81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches:
Indels:
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20
41
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| Qy | Db L   | G                                 | 5 4 4 6 4 8                          |                | DR<br>DR<br>SQ |   | RX<br>RA                           | RA<br>RN<br>RP  | R R O O O O          | OS<br>ON<br>DE  | DT                | AC IO | RE        | DЬ  | γo  | da  | VΩ                              | <u>d</u> d  | 94         | Db                                       | ОУ            | Db &                       |     |  |
|----|--|-----------------------------------|--------------------------------------|----------------|----------------|---|------------------------------------|---|----------------------|---|-------------------|-------|-----------|---|---|---|---------------------------------|---|------------|--|---------------|----------------------------|-----|--|
| ₽  | 10 10 TURNITTCCTTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCTTCAGAAGAA 69 | 0-/3/A-1 (1-375) x Q20246 (1-264) | No.:  nt Similari Local Simil Match: | gnment Scores: |                | "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 28::2012-2018(1998) | MEDITIRE=99069613; PubMed=9851916; | SEMENTER FROM N.A.  MCMUTTAY A.A.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.  SEMENTER TO THE TABLE OF THE | ; Me;<br>he;<br>D=62 | 01-JUN-2002 (TYEMBLIFE). 21, Last annotation update) F40G12.5 protein. F40G12.5. Chemorhab. | EMBLrel. 01, Crea | 0246; | RESULT 13 | 91 AsnLeuAlaTrpAlaLeuAspAsnAlaAspIlaAspCvsG[  I     ::: | 229 AATGTCGTTGATGGTGAAGAGTTAAGAGGTGAAGAGTTAAGAGGTGAAGAA | 71 PheAsnLeuAlaTyrCysTyrSerMetIleAsnAsnAsnAsnSert.com [ | 169 TTCAAGACGGAGTACTGCTACATCGTT | 51 GluLysAlaIleGluMetIleThrLysAlaLeuGluLeuTurcThr | 160yvartys | 31 GluCysLysCysHisSerTyrTyrAsnAlaGlvValc | 151 GAATGCAAA | 11 TyrAsnThrAigasnTvrseras | 2 0 | <pre>lmilarity:     Similarity th:</pre> |

Qy Вр

130 AAGAAG---TCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGC 186

40 LeualaileileSerGlyLysHisGluCysSerLys-----AspTyrAsp 54

55 PheLeuAlaArgAsnLeuIleGlnArgArgGluAlaLeuThrSerGlyLysGluCysPhe 74

226 TACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTT---GTTGTCGACGAAAAAC 282

LeuGluIleValLys---GluGluCysProGluGluLysPheLysLeuIleGluGluAsn 93

283 TTCACGGAA-----AATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCA 336

94 TyrSerGlnLeuValThrLeuLeuThrGlu---LysProLysAspAsnGlyAlaCysThr 112

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δõ 밁 УQ 밁

В

113 AlaproTyrPheGlnLeuGluGiuIleGlu 122

337 GGTACAGGTGACGAGTCAGATGAAGTTGAT 366

09x9s1; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

PRELIMINARY;

PRT;

509 AA.

polysaccharide synthase.

Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaeae; Streptococcus

NCBI\_TaxID-1313;

Lull D., Munoz R., Lopez R., Garcia E.;

"A single gene (tts) located outside the cap locus directs the formation of streptococcus pneumoniae type 37 capsular polygaccharide: type 37 pneumococci are natural, genetically binary strains."; pfam; pr00535; clycos\_transf\_2.

InterPro; IPR001173; Glycos\_transf\_2; 1.

Pfam; pr00535; clycos\_transf\_2; 1.

SEQUENCE 509 AA; 58888 MW; C6C38DZACFAB0D8A CRC64;

Best Local Similarity:

8.46 78.50 44.59% 31.08%

Gaps: Mismatches: Indels: Conservative:

Length: Matches:

509 23 10 30 11

Query Match: percent Similarity:

 $US-09-936-737A-1 (1-375) \times Q9X9S1 (1-509)$ 

Ş 멍 QY

145 CTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGAC 204

94 IleserGluAlaLysLysValIleLeuLeu-----TyrCys------ 105

85 ACGTTTTACGCCGAACAGAAATATACAGACTTCGATAAATCTTTTAAGAAGTCCTCTGAT 144

В QΥ g

Alignment Scores: pred. No.:

| RESULT 15 Q9U2Q4 AC Q9U2Q4 |
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| present Schmilarity: PRT; 550 AA.  907024.  9070 |

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                 Database :
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   16154066 seqs, 8097743376 residues
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Gapop 10.0 , Gapext 1.0
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375
1 atgaagtatttcttgatttc.....atgaagttgatgaagattaa 375
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3093.891 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|                    | O                  | O                  | Result          |
|--------------------|--------------------|--------------------|-----------------|
| ი თ                | ω 4.               | 21                 |                 |
| 50<br>50           | 51.6<br>51.2       | 51.8               | Score           |
| 13.3               | 13.8               | 13.8               | Query           |
| 13.3               | 13.7               |                    | Match           |
| 236                | 721                | 879                | Query           |
| 272                | 881                | 701                | Match Length DB |
| 13                 | 13<br>17           | 17                 | DB              |
| BM163498           | BM165474           | AZ550718           | 1 H             |
| BM166089           | AZ688514           | BM168486           |                 |
| BM163498 EST566021 | BM165474 EST567997 | AZ550718 ENTEM36TF | Description     |
| BM166089 EST568612 | AZ688514 ENTMU22TF | BM168486 EST571009 |                 |

| 117<br>119<br>119<br>119<br>119<br>119<br>119<br>119<br>119<br>119   | 7<br>8<br>9<br>10<br>11<br>12<br>13<br>14<br>15  |
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| 702<br>7139<br>7139<br>753<br>753<br>763<br>790<br>942<br>891<br>891<br>891<br>908<br>8443<br>912<br>912<br>912<br>912<br>914<br>914<br>914<br>914<br>915<br>915   | 27<br>427<br>55<br>56<br>57<br>67<br>67<br>67<br>67<br>67<br>67<br>67  |
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| BM169291 BM602689 BM160442 BM160415 BM160415 BEB46498 BM166415 BH148582 AZ535744 AZ683582 BH149983 BM169710 AZ549980 AZ5549980 AZ554980 AZ554980 AZ554980 AZ554980 AZ554980 AZ554092 BM161274 AZ679713 BM163267 BM163866 BM170559 CNS0181N AZ560099 AZ550256 | BM166886<br>BM163293<br>BM162507<br>BM17376<br>BM171330<br>BM161175<br>BM161175<br>BM166448<br>BM166448<br>BM161293<br>BM170834  |
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| 550<br>550<br>550<br>550<br>550<br>550<br>550<br>550<br>550<br>550   | EST565816 EST565830 EST565030 EST573853 EST573853 EST5656565 EST568565 EST568565   |

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## ALIGNMENTS

|   |  | JOURNAL<br>COMMENT  | ORGANISM REFERENCE AUTHORS TITLE   | ACCESSION VERSION KEYWORDS SOURCE  | RESULT 1 AZ550718/c LOCUS DEFINITION |
|---|--|---|--|--|--------------------------------------|
| Email: bjloftus@tigr.org Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library Seq primer: M13-Forward Class: shotgun High quality sequence start: 25 High quality sequence stop: 801. | Department OI EukaryOTIC GenOmICS The Institute for GenomIc Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 0208 | HM1:IMSS sheared DNA library Unpublished (2000) Contact: Brendan J Loftus | Entamoeba histolytica Eukaryota; Entamoebidae; Entamoeba. 1 (bases 1 to 879) Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica | genomic, DNA sequence.<br>AZ550718<br>AZ550718.1 GI:11176019<br>GSS.<br>Entamoeba histolytica. |                                      |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGATGATGAATTCCAATTAGACGAAGAAGAAGATGATGAAGAAGATGAAGATGAAG 589
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Contact: Jane Cariton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockvili
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                              Cariton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B. Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
                                                                                                                                                                                                                              Plasmodium yoelii yoelii
                                                                                                                                                                                                                                                                                                                                     EST571009 PyBS Plasmodium yoelii yoelii cDNA clone PYCPB36
                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
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/note="Yector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450,). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.
Location/Qualifiers
1. 701
Location/Qualifiers
10. 701
Location/Plasmodium yoelii yoelii"
//db_xref="taxon:73239"
//db_xref="taxon:73239"
//clone="PyEDB36"
//dev_stage="Asexual blood stages"
//dev_stage="Asexual blood stages"
//lab host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors liqated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to HybrilaPa arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was excised from the HybrilaPa vector and plasmid DNA
172 t
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318 AGATGCAGGTAATGCGGCAGGTACAGGTGACGACTCAGATGAAGTTGAAGATTAA 375 572 GGATGAAGATGACGAAGAAGATGAAGATGACGAAGAAGATGAAGATGAAGAAGAAGATGA 631 198 TGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCA 257 258 AGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317 Conservative 13.8%; 0; Score 51.6; DB 13 Pred. No. 0.00044; Mismatches DB 13; 79; Length 701; Indels 0. 0,

BM165474

721 bp mRNA linear EST 04-DEC-2001
EST3657997 PyBS Plasmodium yoelii yoelii cDNA clone PYCMN68 5' end,
mRNA sequence.

N BM165474
BM165474.1 GI:17311155
EST.
Plasmodium yoelii yoelii.
SM Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
E 1 (bases 1 to 721)
S Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Fraser,C.M. and Carucci,D.J.
Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-3319
Fax: 301-838-0208

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 TGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCA 257
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For clone info, please contact the Malaria Research and Reference
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                                                                                                                                Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTMU22TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ688514
                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                             1 (bases 1 to 881)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                          Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                                   Entamoeba histolytica
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Medical Center Dr., Rockville, MD 20850, USA 301 838 0208 301 838 3543
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/dev_stage="Asexual blood stages"
/lab host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4, At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column.
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                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 TAATTGCTTTTGCTTTTGCAGAAGAAATGAACTTGACAACACATTCGATATTGATTTCA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 CATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 CTGAGTTAGATAACGTAGAGCTTTTTGAAGAAGAAATAATGATGAAGATGATGAATTCC 306
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                                                                                                                                                                                                                                                                                                                                                                                                                               125 AAGATGAAGAAGATGAAGAAGATGAAGA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 GTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 TCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAG 343
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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                  Plasmodium yoelii yoelii.

Plasmodium yoelii yoelii

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 236)

Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,

Fraser,C.M. and Carucci,D.J.
                                                                                                                                                                                                                                                                         EST566021 PyBS Plasmodium yoelii yoelii cDNA clone PYCLF94
                                                                                                                                                                                                                                                      mRNA sequence.
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Plasmodium yoelii EST project at TIGR
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// Clone_lib="Entamoeba histolytica Sheared DNA"
// Clone_lib="Entamoeba histolytica Sheared CTIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
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YCLF94 5' end,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 13.3%;
Local Similarity 55.1%;
              Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Elasmodium yoelii yoelii
Elasmodium yoelii yoelii
Lobaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 272)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                        BM166089 272 bp mRNA linear EST 04-DEC-2001 EST568612 PyBS Plasmodium yoelii yoelii cDNA clone PYCNC52 5' end,
Plasmodium yoelii EST project at TIGR
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                                                                                                                                                                                                           mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parasite Genomics Group
The Institute for Genomic Research
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Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA isolated using oligo(dT)-cellulose chromatography, First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated.
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
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Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B., Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
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Parasite Genomics Group
The Institute for Genomic Research
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
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Contact: Jane Carlton
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J. plasmodium yoelii EST project at TIGR
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Contact: Jane Carlton
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Fax: 301-838-0208
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                          Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J. Plasmodium yoelii EST project at TIGR
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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/lab.host="E.coli XI-1 Blue"
/lab.host="E.coli XI-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
/note-"Vector: pAD-GAL4; At 20-25% parasitemia, blood was
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
isolated using the guanidinjum isothiocyanate method, and
isolated using the guanidinjum isothiocyanate method, and
first strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybriZAP vector and plasmid DNA
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1 (bases 1 to 453)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
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           Plasmodium yoelii EST project at TIGR
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The Institute for Genomic Research
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Plasmodium yoelii EST project at TIGR
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Contact: Jane Carlton
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Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-530-9319
                            1 (bases 1 to 580)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
                                                                                               Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blccollected from BALB/cByJ mice infected with Py17XL
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Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 648)
1 (bases 1 to 648)
1 (carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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The Institute for Genomic Research
9712 Medical Center Drive, Rockvill
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Contact: Jane Carlton
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 651)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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Contact: Jane Carl
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The Institute for Genomic Research
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Seq primer: ADF.
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/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
mRNA isolated using oligo(dT) cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
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                                                         Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 667)
                      Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
                                                                                                                                               EST
                                                                                                                                                                                    mRNA sequence.
BM161293
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Contact: Jane Carlton
  Plasmodium yoelii EST project at TIGR
                                                                                                                                                               BM161293.1
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                                                                                                                          Plasmodium yoelii yoelii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 AGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317
EST563816 PyBS Plasmodium yoelii yoelii cDNA clone PYCKD09 5'
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-530-9319
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL
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Best Local Similarity 55.1
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
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//dev_stage="Assaual blood stages"
//dev_stage="Assaual blood stages"
//lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-CAL4; At 20-25% parasitemia, blood was collected from BALB/CBJJ mice infected with Py17XL microcrystalline cellulose collumns. Total RNA was mrited using the guanidinium isothiocyanate method, and First strand cDNA synthesis was completed using a 50 base fmethyl dCTP. After second strand synthesis, uneven adaptors ligated to the blunt ends. The sample was cleaved strential were treated with Pfu DNA polymerase and EcoRI with XhoI and separated on a sephacryl $5.50 column. HybriZAP arms directionately using EcoRI-XhoI cleaved arms directionately using EcoRI-XhoI cleaved arms directionately using EcoRI-XhoI cleaved arms. excised from the HybriZAP vector and plasmid DNA isolated."
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/strain="17xL"
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES
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| 573<br>80.5<br>80.5<br>77<br>75.5<br>75.5<br>75.5<br>75.5  | Score           |        |
| 100.0<br>14.0<br>14.0<br>13.4<br>13.2<br>13.2<br>13.2<br>13.2<br>13.2<br>13.2<br>13.2  | Match Length DB | Ouerv  |
| 1103<br>1147<br>412<br>368<br>418<br>419<br>419<br>419<br>419<br>432   | ength           |        |
| 21<br>13<br>20<br>22<br>21<br>21<br>21<br>21<br>21<br>21<br>21<br>21<br>21   | B               |        |
| AAY94746<br>AAR22950<br>AAW68010<br>ABB69867<br>AAB14260<br>AAY50109<br>AAB14259<br>AAB29108<br>AAR6769<br>AAR98464  | ID              |        |
| Platelet binding i<br>Leech antiplatelet<br>S. frugiperda immu<br>Drosophila melanog<br>Mouse Ice-4 protei<br>Murine caspase-12<br>Mouse Ice-4 protei<br>Murine caspase-12<br>Human interleukin- | 1               |        |
| g i<br>let<br>let<br>let<br>log<br>cei<br>cei<br>cei   |                 |        |

| 15                               | 4 2          | 41                 | 40       | ט<br>פ     | א מ      | υ (<br>7 | y (      | יט נג<br>ביי דע | ى د<br>د           | 3 (                | ა <u>(</u>        | ט נ      | 2 6      | 0 0               | ى د<br>« | 7 0               | ) n  | O t       | 24                 | ) V          | ع د<br>د د         | ٥ <u>د</u> | ) t     | 2 C                | 1 F                | 170     | ָ<br>ק<br>ק        | л 4<br>- 1 | 1 <u>1</u> | , ,     | 111    |  |
|----------------------------------|--------------|--------------------|----------|------------|----------|----------|----------|-----------------|--------------------|--------------------|-------------------|----------|----------|-------------------|----------|-------------------|------|-----------|--------------------|--------------|--------------------|------------|---------|--------------------|--------------------|---------|--------------------|------------|------------|---------|--------|--|
| 67.5<br>67.5                     | 77           | 7                  | 7        | n 0        | n o      | n 0      | 0 0      | 0 00            | α                  | a                  | 00.               | •        | 000      | 0 0               | 6 0      | 0 0               | 0 0  | n c       |                    | 50.          |                    |            | 70      | , c                | 70.5               | 70.5    | ,                  | 7.7        | 71.5       | /1.5    | 73.5   |  |
|                                  | 11.8<br>11.8 |                    |          |            | 11.9     |          |          | 11.9            |                    |                    |                   |          | 12.0     | 12.0              | 12.0     | 12.0              | 12.0 | 12.0      | 12.1               | 12.1         | 12.1               | 12.2       | 12.2    | 12.2               | 12.3               | 12.3    | 12.4               | 12.5       | 12.5       | 12.5    | 12.8   |  |
| 488                              |              |                    |          |            |          |          |          |                 |                    |                    |                   |          |          |                   |          |                   |      | 717       | 3257               | 674          | 674                | 1167       | 669     | 669                | 367                | 156     | 589                | 320        | 256        | 175     | 1154   |  |
| 21 2                             | 21           | 2 2 3              | 22       | 22         | 22       | 20       | 22       | 23              | 22                 | 21                 | 23                | 22       | 22       | 22                | 22       | 22                | 22   | 21        | 22                 | 23           | 19                 | 22         | 23      | 23                 | 22                 | 23      | 22                 | 21         | 21         | 21      | 22     |  |
| AAG34635<br>AAG34635<br>AAG53205 | AAG34636     | ABP00862           | AAM78435 | AAM39516   | ABG07270 | AAY41665 | AAB94657 | ABB08153        | ABB58651           | AAB18176           | ABG61879          | AAM41085 | AAM41084 | AAB94096          | AAM39299 | ABB11943          |      |           |                    |              |                    |            | ABB0978 | ABB0977            | ABB7195            |         | AAB95086           |            | AAG1778    | AAG1778 | ABB669 |  |
| is                               | dopsis       | Human ORFX protein | dArod    | human diag | , ≌      | n protei | PLA2     | iila            | Plasmodium falcipa | Prostate cancer-as | Human polypeptide | polypep: |          | Human polypeptide |          | Human polypeptide | ORFX | Phila me. | S. pneumoniae Sp11 | treptococcus | Hericobacter pylor |            | acid    | prosophila melanog | Lung small cell ca | n prote | Flasmodium falcipa | S          | _          | melano  |        |  |

### ALIGNMENTS

RESULT 1

AAY94746 WPI; 2000-611629/58. N-PSDB; AAA28180. Scheuble B; Strittmatter W, Guessow D, (MERE ) MERCK PATENT GMBH. 18-MAR-1999; 12-MAY-1999; 10-MAR-2000; 2000WO-EP02117. Saratin; medicinal leech; thromboembolic disease; intraocular lens; collagen-dependent platelet adhesion inhibition; posterior capsule opacification. WO200056885-A1. Hirudo medicinalis. Platelet binding inhibitor protein Saratin amino acid sequence. 28-SEP-2000. 29-JAN-2001 (first entry) AAY94746 standard; Protein; 103 AA. AAY94746; 99EP-0105530. 99EP-0109503. Hofmann U, Hemberger J, Fotev 2;

Page 2

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cc encoding Saratin, an expression vector comprising the DNA sequence, a constraint of the DNA sequence and cc immunospecific for Saratin, and methods for identifying Saratin agonists cor antagonists. Saratin is useful for treating thromboembolic processes, and for manufacturing a medicament for treating thromboembolic processes. Cc and for manufacturing a medicament for treating thromboembolic diseases. Saratin is also useful for coating artificial surfaces, since use of Saratin renders them cc for coating artificial surfaces, since use of Saratin renders them cc mon-adhesive for cells and prevents the activation of cells. It may also useful for modifying intraocular lenses in order to lessen the cc useful for modifying intraocular lenses in order to lessen the lens material for covalent crosslinking to modify the lens material. The lens material cc is used for refractive anterior or posterior chamber ocular implants, cc which may be implanted into the eye. This new type of coating avoids to be used in the complete of the combination with other problems contributed by stimulated cell growth. In combination with other complete to coating avoids and the coating avoids to the complete of the coating avoids to coating the coating the coating avoids to coating the coating t
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR22950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Saratin polypeptide and gene isolated from Hirudo medicinalis for blocking platelet adhesion, especially useful for treating or preventing thrombotic diseases, or for manufacturing a medicament for preventing thrombotic diseases, or for manufacturing a medicament for preventing thrombotic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saratin is a protein isolated from the saliva of the medicinal leech Hirudo medicinalis. Saratin is an inhibitor of collagen-dependent platelet adhesion. The invention includes polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 41; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thromboembolic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            helps to completely overcome posterior capsule opacification. The antibody immunospecific for Saratin, as well as Saratin itself, are useful for measuring samples derived from host cell cultures or from a useful subject. The present sequence represents the amino acid sequence for the center of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAPP; collagen; platelet aggregation; antithrombotic; anticoagulant; coronary artery disease; cerebrovascular disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR22950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leech antiplatelet protein.
                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haementeria officinalis
                                         15-APR-1992.
                                                                                                               EP480651-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EELDQEKFYVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EELDQEKFYVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Saratin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EEREDCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EEREDCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103;
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                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                        /label= leader_peptide
/note= "21 hydrophobic
                                                                                                                                                                                                      /label- mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 573; DB 21; 100.0%; Pred. No. 2.3e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                 amino acids"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 3
AAW68010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            When cloned into the yeast expression vector pKH4a2, the LAPP gene sequence forms a fusion product of MAF-alpha-1 leader sequence plus mature LAPP, which when produced are proteolytically processed by plus mature LAPP, which when produced are proteolytically processed by the Lys-Arg cleaving endopeptidase (KEX2), which cleaves on the the Lys-Arg cleaving endopeptidase (KEX2), which cleaves on the culture craminal side of Lys-Arg, and the products secreted into the culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ23682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Connolly TN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein to inhibit collagen simulated platelet aggregation extracted from salivary gland of Haementeria officinalis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-125288/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAPP blocks stimulation of platelet aggregation by collagen, at an antithrombotic concentration of about 100 nMolar (or 1.6 ug/ml). antithrombotic stimulated by 2 ug/ml collagen and addition platelet aggregation is stimulated by 2 ug/ml collagen and addition of LAPP inhibits this with an IC50 of 45nM, but this may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 15; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overcome by the addition of 0.25 mM arachidonic acid. LAPP could be used for treatment and prevention of thrombotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conditions especially coronary artery and cerebrovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAQ23871-7.
                                                                                                                                                                                                                                                                                                                                                                                                AAW68010 standard; Protein; 412 AA.
                                                                                                                                                                                                                                                                                                        S. frugiperda immunophilin FKBP46.
                                                                                                                                                                                                                              spodoptera frugiperda.
                                                                                                                                                                                                                                                           transplant; tissue graft.
                                                                                                                                                                                                                                                                        Immunophilin; moth; insect cell; nuclear; immunosuppression; drug;
                                                                                                                                                                                                                                                                                                                                        27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                      AAW68010;
                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match
Local Similarity 32.7%; Pred. No. 1.1;
Local Similarity 32.7%; Pred. No. 1.1;
hes 18; Conservative 10; Mismatches 24; Indels 3.
                                                                                          Domain
                                                                                                                                                     Region
                                               Domain
                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 DCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRN 120
                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 DCWTTYANRKYTDEDKSFKKSSDLDECKKTCFKTEY---CYIVFEDTVNKECYYN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombotic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keller PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0594917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91EP-0309157.
                                                                                                                                                                                                                                                                                                                                          (first entry)
                   /note= "EEAP motif" 219..223
                                                              /note= "putative nuclear localisation signal"
/note= "AP motif"
                                                                                                                                                                      /note= "EEAP motif"
                                                                                                                                                                                                   Location/Qualifiers
    /note= "putative nuclear localisation signal"
                                                    215..218
                                                                                                          /note= "putative nuclear localisation signal"
                                                                                                                                        note= "putative nuclear localisation signal"
                                                                                                                                .138
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Domain Region Region

Region

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(UYJE-) UNIV JEFFERSON THOMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the immunophilin FKBP46 from the moth Spodoptera fruglperda. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that can be used to study and identify additional immunosuppressive bind to it. Such immunosuppressive agents can be used in treating transplant and tissue graft patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           ABB69867 standard; Protein; 368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 ANKKAKPDKKAGKNSAPAAESDSDDDD------EDQLQK-----FLDGEDIDT 174
                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                          prosophila melanogaster polypeptide SEQ ID NO 36393.
                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 DE--NDESFKMN--TSAEGDDSDEEDDDEDEEDEEDDD 208
                                                                                                                               pharmaceutical.
                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ANRKYTDEDKSEKKS-----SDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ 65
WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-130433/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fernandes-Alnemri T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0741134.
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298..30
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                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%; Score 80.5; Di
30.6%; Pred. No. 3.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "putative nuclear localisation signal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
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                                                                                                                                                                                                                                                                                                      AAB14260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA discloses (ABL01840-ABL16175) and the encoded proteins sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _{\rm New} isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABL13970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification, but was obtained in electronate fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB14260 standard; Protein; 418 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ced-3; virally induced cell death; apoptosis; gene therapy; neural; muscular degenerative disease; myocardial infarcation; stroke; aging; interleukin-lbeta converting enzyme; ICE; cysteine protease; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB14260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 --LDKLRAVATSSDSDENYNKSSSPDLALDLHASDVEADVDGDEAGDADEDGDADAD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Ice-4 protein sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 KYTDFDKS-----FKKSSDLDECKKTCFKTEYCYIVFE---DTVNKECYYNVVDG 60
                                                                                                                                                                                                                                                                                                                                                                                                            ds snw
                                                                                                                                                                                                                                                                                                                                              US6083735-A.
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                                                                                                                                                                                                                                                                         04-JUL-2000.
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                                                                                                                                                                                                               10-JUN-1994;
                                                                                                                                          24-JUN-1993;
          Yuan J,
                                                                     (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EELDQEKFVV-----DENFTEN-----YLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYTDADESVSAPTEFLAEFLSAVMLKDYKKA---LKYCKLILQYEPDNATAKEFYPLI-- 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 AA;
                  Miura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                        93US-0080850
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23.9%; pred. No. 7.8;
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 368;
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Query Match Matches

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ABB69867;

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Alnemri ES,

31-OCT-1996; 19-JAN-1999 US5861498-A

The invention is

01-NOV-1995;

31-OCT-1996;

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RESULT 6
AAY50109
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                        (GEHO ) GEN HOSPITAL CORP.
                                                     16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                              14-APR-1999;
                                                                                                       21-OCT-1999.
                                                                                                                              W09952925-A1.
                                                                                                                                                     Cleavage-site
                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                       Caspase; splice variant; truncated; programmed cell death; apoptosis; regulation; proteolytic cascade; malignant condition; cancer; premailignant condition; solid tumour; lymphoma; chronic lymphocytic leukaemia; prostatic hypertrophy;
                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                                                                                                                 preneoplastic liver focus; chemotherapy resistance;
                                                                                                                                                                                                                                                                                                                             Murine caspase-12 splice variant, caspase-12L.
                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              AAY50109;
                                                                                                                                                                                                                                                                                                                                                                                                          AAY50109 standard; Protein; 419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a mouse Ice-4 protein sequence. The present sequence was used in a sequence homology comparison with the protein sequences of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14246). The coding sequence of the present sequence is a member of a family of genes involved in programmed cell death (apoptosis). Ich-1 may play an important role in both the positive and negative regulation of apoptosis. The Ich gene muscular degenerative diseases, myocardial infarcation, stroke, virally induced cell death and aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 DE-----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 17; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 VEDDLYEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human Ich-1L and Ich-1S proteins for negative and positive regulation of programmed cell death and for developing therapeutic methods for diseases and conditions characterized by cell death, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-464343/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
  Morishima N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 AA;
                                                 98US-0081962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                        99WO-US08064.
                                                                                                                                                        95..419
/note= "Caspase-12"
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels
                                                                                                                                                                                                                                             autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 418;
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PN XX PF N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB14259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC This sequence represents a cDNA encoding murine caspase-12L, a splice CC variant of caspase-12. Caspases are a family of proteins involved in CC the regulation of apoptosis and are synthesised as proforms which are cactivated via cleavage after specific Asp residues. Mammalian cells carried express several caspases, and it is thought that these act in a cells composed caspase-12S (AR32644) or truncated forms of caspase-12L (AR32644) are used for production, recombinantly or in vivo, caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy), or compared caspase-12 prophastic liver foci and resistance to chemotherapy, or compared caspase-12 prophastic liver foci and resistance to chemotherapy, or compared caspase-12 prophastic liver foci and resistance to chemotherapy, or compared caspase-12 prophastic liver foci and resistance to chemotherapy, or compared to the caspase-12 prophastic liver foci and resistance to chemotherapy.
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                                                Yuan J, Miura M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                       24-JUN-1993;
                                                                                                                                                                              10-JUN-1994;
                                                                                    (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                           04-JUL-2000.
                                                                                                                                                                                                                                                                                                                                      ced-3; virally induced cell death; apoptosis; gene therapy; neural; muscular degenerative disease; myocardial infarcation; stroke; aging;
                                                                                                                                                                                                                                                                       US6083735-A.
                                                                                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse Ice-4 protein sequence #1.
                                                                                                                                                                                                                                                                                                                     interleukin-1beta converting enzyme; ICE; cysteine protease; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14259 standard; Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB14259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 DE-----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 VFEDTVNKECYKNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding the short form of caspase-12, used e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ32645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                9308-0080850
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                                                                                                                                                                         94US-0258287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.2%; Score 75.5; DB 20; Length 419; 35.6%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches 14;
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N-PSDB; AAA72843

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a mouse Ice-4 protein sequence. The present sequence was used in a sequence homology comparison with the protein sequences of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine sequences of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14246). The coding sequence of the present sequence is a member of a family of genes involved in programmed present sequence is a member of a family of genes involved in both the cell death (apoptosis). Ich-1 may play an important role in both the positive and negative regulation of apoptosis. The Ich gene may be used positive and negative regulation of apoptosis. The Ich gene may be used in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders characterised by cell death e.g. neural and in gene therapy in disorders chara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 16; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    induced cell death and aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB29108 standard; protein; 419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; caspase-12; calpain; apoptosis; cell death; autoimmune disease; cancer; viral infection; apoptotic condition; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine caspase-12 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             дав29108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2000; 2000WO-US09173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                            Caspase-12 polypeptide useful for treating apoptotic conditions e.g. stroke, ischemia and proliferated disease e.g. cancer, lacks at least 5 amino acids in a specific region of the native amino acid sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200059924-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 VEEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 EQLSLQFSNDEDD 94
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                                                                                                                                                                                                                                                                                                         WPI; 2000-679352/66.
The present invention is concerned with methods for identifying compounds useful for modulating caspase-mediated apoptosis. These include the caspase-12 protein shown here. These agents can be used in the treatment
                                                                                                                      Claim 1; Page 65-66; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                   Yuan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE-----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                Nakagawa T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0127967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AAR66769
ID AAR6
                                                                                                                                                                                                                                                                                                                                               RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of apoptotic conditions, including stroke, neurodegeneration, ischaemia, all pheimer's disease and muscular dystrophy, and proliferative diseases such as cancer, autoimmune disorders such as systemic lupus erythematosus and multiple sclerosis, and viral infections, particularly those associated with herpes virus, poxvirus and adenovirus. The treatment may associated with herpes virus, poxvirus and adenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be in the form of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR66769 standard; Protein; 432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oncogene bc1-2; programmed cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human interleukin-1 beta convering enzyme homolog (Ice-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR66769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human interleukin-1 beta converitng enzyme homolog; Ice-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9500160-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                          AAQ79969 encodes AAR66769 human interleukin-1 beta converting enzyme homolog (Ice-4), increasing Ice-4s enzymatic activity can homolog (Ice-4), increasing Ice-4s enzymatic eclis (pref. those promote the programmed cell death of cancer cells (pref. those overexpressing the bcl-2 oncogene), this can be used as the basis of a new cancer treatment. Alternatively by reducing Ice-4s enzymatic of a new cancer treatment. Alternatively by reducing the be useful activity programmed cell death can be inhibited, this may be useful activity programmed cell death can be inhibited, this may be useful activity programmed cell death can be inhibited, this may be useful activity programmed cell death can be inhibited, this may be useful activity programmed cell death can be inhibited, this may be useful activity programmed cell death can be inhibited, this may be useful activity programmed cell death can be inhibited.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSO 81
                                                                                                                                                                                                                                                                                                   promoting or preventing programmed cell death in vertebrate cells - by inhibiting the activity of interleukin-1 beta converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 DE-----SDEVD 101
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                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ79969
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-051742/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                        Claim 24; Fig 16; 116pp; English.
                                                                                                                                                                                                                                                                                       enzyme.
Sequence
                                          for extended or indefinite periods, independant of growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Yuan J;
           432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0080850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US06630
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35.6%; Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
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Query Match Best Local Similarity

Conservative

14;

Mismatches

13.2%; Score 75.5; 35.6%; Pred. No. 14;

DB 16; 14;

Length 432;

19;

Gaps

6

Matches

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RESULT 11
ABB66916
                                                                                                                                                                      Query Match
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AAR98464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                         Ich-3 (AAR98464) causes programmed cell death and shows significant homology to mouse interleukin-1 beta converting enzyme (ICE), mouse mich-2 (AAR98461) and human Ich-1 (AAR98462-63). Its sequence was deduced from the Ich-3 gene (AAR931554) isolated from a mouse thymus cDNA library. The protein can be obtd. from host cells contg. vectors that include an Ich-3 coding sequence. It can be used to control the programmed cell death of vertebrate cells, to develop cell control the programmed cell death of vertebrate cells, to develop cell
                                                                                                                                                                  Sequence
                                                                                                                                                                                  lines that remain viable for extended periods, and to increase the
                                                                                                                                                                                                                                                                                       Claim 24; Fig 14; 127pp; English.
                                  96 EQLSLQFSNDEDD 108
                                                       95 DE-----SDEVD 101
                                                                                                                                                                                                                                                                                                               Preventing or promoting programmed cell death in vertebrate cells comprises inhibiting or increasing the activity of interleukin-1-beta converting enzyme, or altering expression of
                                                                 40 VEDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 95
                                                                                    44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT31554
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-333763/33.
                                                                                                                                                                                                                                                                                                                                                                                                  Miura M, Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ich-3; murine ICE-ced-3 homologue; programmed cell death;
apoptosis; interleukin-1 beta converting enzyme; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9620721-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine Ich-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR98464 standard; Protein; 432 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 DE-----SDEVD 101
                                                                                                                                                                432 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0368704
                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US00177
                                                                                                             13.2%; Score 75.5; DB 17; 35.6%; Pred. No. 14; tive 14; Mismatches 14;
                                                                                                                                  DB 17; Length 432;
                                                                                                              Indels
                                                                                                            19;
                                                                                                           Gaps
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Вb Ş 멍 Ωy

Protein identification; signal transduction pathway; metabolic pathway;

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RESULT 12
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Arabidopsis thaliana protein fragment SEQ ID NO: 18943.
                                                                                                            AAG17789;
                                                                                                                                     AAG17789 standard; Protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention of discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01840-ABL10175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                      565 LVENFWRHYIQCCECQKKDACALSNPSMLGNTEYTG 600
                                                                                                                                                                                                                                                                                                             505 SKKDIDESKFESMLDDKDKLKERVAELMVRCMFLMEKRMOODLKGNKVCNVEEKDNNVNO 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 27540; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                  70 VDENFTENYL--TDCEGKDA-----GNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                       12 NRKYTDFDKSFKKSSDLDECK-KTCFKTEYCYIVFEDTVNKECYYN-VVDGEELDQEKFV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 27540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB66916 standard; Protein; 1154 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1154 AA;
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                   12.8%; Score 73.5;
28.1%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                         42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1154;
                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  4,
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| יי סי סי סי סי סי סי סי מי  | יים סיסיסיסיסיסיסיסיסיסיסיסיסיסיסיסיסיסי   | א א א א א א א א א א א א א א א א א א א  | S R R R R R R R R R R R R R R R R R R R  |
|---|--|--|--|
| 18 JUN 1999<br>18 JUN 1999<br>18 JUN 1999<br>18 JUN 1999<br>18 JUN 1999<br>18 JUN 1999<br>21 JUN 1999<br>22 JUN 1999<br>23 JUN 1999<br>23 JUN 1999  | 27-MAY 1999; 27-MAY 1999; 01-JUN-1999; 03-JUN-1999; 04-JUN-1999; 07-JUN-1999; 07-JUN-1999; 10-JUN-1999; 110-JUN-1999; 110-JUN-19   | 23-APR-1999 28-APR-1999 30-APR-1999 30-APR-1999 30-APR-1999 04-MAY-1999 06-MAY-1999 06-MAY-1999 11-MAY-1999  | hybridisation stermination s<br>Arabidopsis t<br>EP1033405-A2.<br>06-SEP-2000.<br>25-FEB-2000;<br>25-FEB-1999;<br>05-WAR-1999;<br>09-WAR-1999;<br>25-WAR-1999;<br>25-WAR-1999;<br>25-WAR-1999;<br>26-APR-1999;<br>01-APR-1999;<br>01-APR-1999;<br>01-APR-1999;<br>01-APR-1999;<br>01-APR-1999;<br>01-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999;<br>11-APR-1999; |
| 9908 - 0139460<br>9908 - 0139461<br>9908 - 0139462<br>9908 - 0139463<br>9908 - 0139463<br>9908 - 0139750<br>9908 - 0139763<br>9908 - 0139817<br>9908 - 013989<br>9908 - 0140353<br>9908 - 0140354 | 990S-0136392<br>990S-0136782<br>990S-013722<br>990S-0137528<br>990S-0137502<br>990S-0137502<br>990S-0137502<br>990S-013904<br>990S-0138540<br>990S-0138647<br>990S-013919<br>990S-0139452<br>990S-0139453<br>990S-0139455<br>990S-0139455<br>990S-0139455<br>990S-0139456<br>990S-0139456  | 99US-0130510. 99US-0131449. 99US-01324048. 99US-0132407. 99US-0132485. 99US-0132485. 99US-0132487. 99US-0132487. 99US-0132487. 99US-0132487. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134218. 99US-013421. 99US-013421. 99US-013421. 99US-013421. 99US-013421. 99US-013421. 99US-013421. 99US-013421. 99US-013421. 99US-013423. | n assay; genetic mapping; sequence.  thaliana 2000EP-0301439. 299US-0121825. 99US-0125848. 99US-0125788. 99US-012664. 99US-0126785. 99US-0126785. 99US-0126785. 99US-0128714. 99US-0128344. 99US-0130077. 99US-0130077.  |
|   |  |  | gene expression  |
|   |  |  | control; promoter;   |
| חד חד עד מי   |  |  |  |
| 03888888888   | 변화 등 한 한 한 한 한 한 한 한 한 한 한 한 한 한 한 한 한 한   |  | ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק ק  |
| 1991  | VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG-199<br>VG | 1991199  | 24-JUN-1999; 28-JUN-1999; 30-JUN-1999; 01-JUL-1999; 01-JUL-1999; 02-JUL-1999; 06-JUL-1999; 06-JUL-1999; 11-JUL-1999; 12-JUL-1999; 11-JUL-1999;  |
| 014<br>014<br>015<br>015<br>015<br>015<br>015   | 014<br>014<br>014<br>014<br>014<br>014<br>014<br>014<br>014<br>014   | 014<br>014<br>014<br>014<br>014<br>014<br>014<br>014<br>014<br>014   | 99US-0140695. 99US-0140823. 99US-0141287. 99US-0141287. 99US-0142154. 99US-0142390. 99US-0142920. 99US-0143624. 99US-0144085. 99US-0144333. 99US-0144333. 99US-0144333. 99US-0144333.  |

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RESULT 13
AAG17788
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Query Match
Best Local S
Matches 26
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11-SEP-1999
13-SEP-1999
15-SEP-1999
26-SEP-1999
27-SEP-1999
28-SEP-1999
28-SEP-1999
29-SEP-1999
04-OCT-1999
06-OCT-1999
08-OCT-1999
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28-OCT-1999
29-OCT-1999
                protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                             Arabidopsis
                                                                17-OCT-2000 (first entry)
                                                                                    AAG17788;
                                                                                                     AAG17788 standard; Protein; 256 AA
        termination sequence.
                                                                                                                                                    93
                                                                                                                                                                                                     KKGS-----KRALPEESFFTWFTDAQHKE-----DAGDEIHDEVADIIKEDLWSNPLTY 141
                                                                                                                                                                                                                               Similarity
26; Conservat
                                             thaliana
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                    990S-0152363

990S-0153768

990S-0154018

990S-0154039

990S-0155659

990S-0155659

990S-0155659

990S-015717

990S-015717

990S-015717

990S-015832

990S-015832

990S-0159294

990S-0159330

990S-0159330

990S-0159331

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990S-0159331

990S-0159331

990S-0159331

990S-0160767

990S-0160767

990S-0160763

990S-0160763

990S-0160763

990S-0160763

990S-0161361

990S-0161406

990S-0161361

990S-0161361
                                                                                                                                                                                                                                        12.5%;
                                             protein fragment SEQ ID NO: 18942.
                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                              score 71.5; DE
Pred. No. 12;
12; Mismatches
                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                  Length 175;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                               80
                                                                                                                                                                                                                                 4;
 25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-AFR-1999
01-AFR-1999
16-AFR-1999
119-AFR-1999
21-AFR-1999
23-AFR-1999
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25-AFR-1999
30-AFR-1999
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30-AFR-1999
30-AFR-1999
20-MAY-1999
21-MAY-1999
24-MAY-1999
25-MAY-1999
27-MAY-1999
28-MAY-1999
01-JUN-1999
01-JUN-1999
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11-JUN-1999
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13-JUN-1999
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06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                18-MAY-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1999;
14-MAY-1999;
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990S-0132048

990S-0132487

990S-0132485

990S-0132486

990S-0134218

990S-013421

990S-013421

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990S-0135124

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990S-0139454

990S-0139453

990S-0139463

990S-0139463
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99US-0123180.
99US-0125748.
99US-0125788.
99US-0126264.
99US-01267465.
99US-0128234.
99US-0128234.
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S-0130077.
S-0130449.
S-0130510.
S-0130891.
S-0131449.
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RESULT 14
AAB18263
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Best Local s
Matches 26
                                   Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
      W0200025728-A2
                          Plasmodium falciparum.
                                                                   Plasmodium falciparum chromosome 2 related protein SEQ ID NO:120.
                                                                                              07-NOV-2000 (first entry)
                                                                                                                                      AAB18263 standard; Protein; 320 AA.
                                                                                                                                                                                                                                                                                                                                                     14-OCT-1999
14-OCT-1999
14-OCT-1999
18-OCT-1999
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26-OCT-1999
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16-SEP-1999

20-SEP-1999

22-SEP-1999

23-SEP-1999

24-SEP-1999

28-SEP-1999

29-SEP-1999

04-OCT-1999

05-OCT-1999

06-OCT-1999

07-OCT-1999

07-OCT-1999

13-OCT-1999

13-OCT-1999
                                                                                                                                                                                         | :| | : | | : | :| 253 FNNDADEEDFDGDDDGDEEGEEDDDDEEEED 253
                                                                                                                                                                                                                            174 KKGS-----KRALPEESFFTWFTDAQHKE-----DAGDEIHDEVADIIKEDLWSNPLTY 222
                                                                                                                                                                                                                                                                                                                                   28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                   81 -----DCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                        23 KKSSDLDBCKKTCFKTEYCYIVFEDTVNKECYYNVVDGBEL-DQEKFVVDENFTENYLT- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-1999;
13-OCT-1999;
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                   990S-0154018

990S-0154079

990S-0155479

990S-0155659

990S-0155659

990S-0157117

990S-0158029

990S-0158232

990S-0158232

990S-0158232

990S-0158233

990S-0159234

990S-0159234

990S-0159233

990S-0159330

990S-0159331

990S-0159331

990S-0159638

990S-0160741

990S-0160768

990S-0160768

990S-0160814

990S-0160814

990S-0160814

990S-0161406

990S-0161406

990S-0161361

990S-0161361
                                                                                                                                                                                                                                                                                    12.5%; Score 71.5;
28.6%; Pred. No. 19;
                                                                                                                                                                                                                                                                     12; Mismatches 32; Indels 21;
                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                          Length 256;
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990S-0142154
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16-JUL-1999; 16-JUL-1999; 19-JUL-1999;

13-JUL-1999; 14-JUL-1999; 15-JUL-1999;

22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 26-JUL-1999 26-JUL-1999 27-JUL-1999 28-JUL-1999 28-JUL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. By chromosome 2 of the human malarial parasite, Plasmodium falciparum. Valso described are: (1) nucleotide sequences (II) encoding (I); and (2) and (II) are useful for the development of vaccines against (I) and (II) are useful for the development of vaccines against (I) and polyclonal antisera or a monoclonal p. falciparum infection. (I) and polyclonal antisera or a monoclonal p. falciparum infection (I) and polyclonal antisera or a monoclonal p. falciparum fundopens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequence of (I), are antibody raised to immunogens comprising the sequence of (I), are antibody raised to immunogens comprising the sequence of (I), and (I) and (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of p.falciparum infection –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 283-284; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoffman S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p. falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for complexity of the parasitic lifecycle, and provide new targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                             AAB95086 standard; Protein; 589 AA
                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                           Human protein sequence SEQ ID NO:16999.
                                                                                                                                                                                                                                                                              AAB95086;
EP1074617-A2
                                                                                                                                                                                                                      26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 DEVYIIYEYMENDSIL-----KFDEYFFVLDKNYT 140
                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 ---YIVFEDTVNKECYYNVVDGEELDQEKFVVDENFT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 FYALKKYEKSLLEKKRDFTKSNNDKISIKSKYDDFKNELQIITDIKNEYCLTCEGIITNY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 FYANRKY-----TDFDKS----FKKSSDLDECKK-----TCFKTEYC------ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 AA;
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27-AUG-1999;
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence and an oligonucleotide comprising a sequence, where the polynucleotide which comprises a 3'-end sequence, where the combination of oligonucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence', are discussed in antisense therapy and the specification. The primer sets can be used in antisense therapy and the specification. The primer set useful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, in gene therapy full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by detection and/or diagnosis of the abnormality of the proteins encoded by detection and/or diagnosis of the primers allow obtaining of the full-length the full-length cDNAs. The primers allow obtaining of the full-length the stall of the stall of the primers and AAH13628 and AAH13633 to AAH13640 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 AAB95893 represent human amino acid sequences; and AAH13630 to the primers are used in the exemplification of the primers 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of a polynucleotide comprise of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 16999; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the present invention.
                                                                                                  218 MTRDSDGYENSTDGEMCDKDALEEDSESVSEIGSDESENEITSV-GRASGDDDGSEDDE 276
                                                                                                                                                                                                                 158 SKEFTQKNKKEKKNIVQHTTDSSLEEKQRTLDSGTSEIVKTPRIECSKTRREMQSVVQLI 217
     277
                                                                                                                                                                                                                                                                     12 NRKYTDEDKSEKKS-----SDLDECKKT------CEKTE---YCYIVEE 46
                                                                                                                                                            47 DTVNKECYYNVVDGEELDQEKFVVD-----ENFTENYLTDCEGKDAGNAAGTGDES 97
                                                       98 DEVDED 103
  EE-DED 281
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                         12.4%; Score 71; DB 23.8%; Pred. No. 59;
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                                                                                                                                                                                                                                                                                                                                     23; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 589;
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X, Otsuki T;
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Search completed: February 25, 2003, 02:32:13

time

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Result
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Match Length
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-813-940-25
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US-08-88-497-38
US-09-362-230-38
PCT-US94-07926-38
                                                                                                              US-08-044-547-3
US-08-044-547-1
US-08-041-134-2
US-09-187-789-16
US-09-187-789-16
US-09-139-600-11
US-08-368-704C-56
US-08-368-704C-56
US-08-368-704C-56
US-08-368-704C-59
US-08-368-704C-59
US-08-368-704C-59
US-08-368-704C-59
US-08-888-704C-59
US-08-888-704C-59
US-08-888-497-41
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| 61.5              | 61.5              | 61.5              | 61.5              | 61.5            | 62.5             | 62.5              | 62.5            | 62.5            | 6.5             | 63               | 5 6               | 5 6              | 63                | 0                | 64               | 64.5              | 64.5              |
| 10.7              | 10.7              | 10.7              | 10.7              | 10.7            | 10.9             | 10.9              | 10.9            | 10.9            | 10.9            | 11.0             | 11.0              | 11.0             | 11.0              | 11.0             | 11.2             | 11.3              | 11.3              |
| 416               | 416               | 416               | 346               | 346             | 2555             | 1172              | 250             | 250             | 250             | 1726             | 1726              | 1658             | 1658              | 294              | 519              | 148               | 148               |
| 4                 | ω                 | N                 | N                 | N               | ω                | ۳                 | w               | Ν               | N               | 4                | N                 | 4                | N                 | 4                | 4                | G                 | 4                 |
| US-09-468-442-3   | US-09-340-993-3   | US-09-211-930-3   | US-08-702-153-4   | US-08-702-153-2 | US-09-058-489-36 | US-08-313-288B-19 | US-09-293-273-5 | US-09-134-596-5 | US-08-861-269-5 | US-09-170-996-30 | US-08-609-049A-30 | US-09-170-996-13 | US-08-609-049A-13 | US-09-355-160D-8 | US-09-172-841-55 | PCT-US94-07926-36 | US-09-362-230-36  |
| Sequence 3, Appli | Sequence 3, Appli | Sequence 3. Appli | Sequence 4. Appli | ٥               | , א<br>ה         | Sequence 19 Appl  | υĺ              | л               | л               | ω .<br>Ο .       | 30                |                  | <u></u>           | ω                | 55               | Sequence 36, Appl | Sequence 36. Appl |

#### ALIGNMENTS

RESULT 1 US-08-044-547-3

Sequence 3, Application US/08044547 Patent No. 5324715

GENERAL INFORMATION:

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US-08-044-547-3
                                                                                                                                                      TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
Best Local Similarity Matches 18; Conserv
                                  Query Match
                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/594,917
FILING DATE: 09-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: PAIR: Richard S.
REGISTRATION NUMBER: 32,586
REFERENCE/DOCKET NUMBER: 18053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Connolly, Thomas M.
APPLICANT: Keller, Paul M.
TITLE OF INVENTION: Protein for Inhibiting
TITLE OF INVENTION: Collagen-Stimulated Platelet Aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                         TOPOLOGY:
                                                                                                                                               TYPE:
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CITY: F
                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Jersey
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                                                                                                         unknown
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                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                          unknown
         14.0%; Score 80.5; DB 1; Length 126; 32.7%; Pred. No. 0.21;
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Conservative

10; Mismatches

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Gaps

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DCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEY---CYIVFEDTYNKECYYN 56

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US-08-044-547-1
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                                                                                                                                                                                                                                              RESULT 3
US-08-741-134-2
                                                                                                                                                                                                                                                                                                                                   밁
GENERAL INFORMATION:
APPLICANT: Litwack, Gerald
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Fernandes-Alnemri, Teresa
TITLE OF INVENTION: IMMUNOPHILIN FKBP46
TITLE OF INVENTION: METHODS OF USING TH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                Sequence 2, Application US/08741134 Patent No. 5861498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Parr, Richard S.
REGISTRATION NUMBER: 32,586
REFERENCE/DOCKET NUMBER: 1805
REFERENCE/DOCKET NUMBER: 1805
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Connolly, Thomas M.
APPLICANT: Keller, Paul M.
TITLE OF INVENTION: Protein for Inhibiting
TITLE OF INVENTION: Collagen-Stimulated Platelet Aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-OCT-1990 ATTORNEY/AGENT INFORMATION: NAME: Parr, Richard S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 DCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYTLQINTETNECYRN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 07065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                 66 DCWSKRPGWKLPDNLLTKTEETSVDECRKMCEESAVEPSCYILQINTETNECYRN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/594,917
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            5 DCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEY---CYIVFEDTVNKECYYN 56
                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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P.O. Box 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%; Score 80.5; DB 1; Length 147; 32.7%; Pred. No. 0.25;
                                                METHODS OF USING THE SAME
                                                                                           IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/044,547
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GENERAL IMFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION UNMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 172
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             Qy
                                                                                                                                          ; ORGANISM: Mus musculus US-09-187-789-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09187789 Patent No. 6340740
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                                                                           Query Match
Best Local Similarity
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                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 3.11 SOFTWARE: WordPerfect for Windows 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 ANKKAKPDKKAGKNSAPAAESDSDDDD------EDQLQK-----FLDGEDIDT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5861498ris
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 DE--NDESFKMN--TSAEGDDSDEEDDDEDEEDEEDDD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 6 FILING DATE: 01-NOV-1995 CLASSIFICATION: 424
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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             44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                         26; Conservative
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)GY: linear
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                                                                                13.2%; Score 75.5; DB 4; Length 172; 35.6%; Pred. No. 1;
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                                                            14; Mismatches 14;
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHOD OF USE
TILE REFERENCE: 480140.434
TILE REFERENCE: 480140.434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-258-287B-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/139,600 CURRENT FILING DATE: 1998-08-25 NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 58, Application US/08258287B Patent No. 6083735 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 DE-----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 VEDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 VEEDTVNKECYYNVVDGEEL----DOEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
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                                                         APPLICATION NUMBER: US 08 FILING DATE: 24-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        CURRENT APPLICATION DATA:
NAME: BUGALSKY, LAWFENCE B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 060
REFERENCE/DOCKET NUMBER: 060
                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      STREET: LIVE CITY: Washington
                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                 STATE: D.C
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 10-JUN-1994
                                                                                                                                                                                         SOFTWARE:
                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Conservative
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                                                                                                                                                                                                                                                                                                                                 3: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                       Floppy disk
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                                                                                                      US 08/080,850
                                                                                                                                                              US/08/258,287B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75.5; DB 4; Length 172; pred. No. 1;
                            0609.3920001
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US-08-258-287B-58
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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GENERAL INFORMATION:

APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
APPLICANT: Miura, Masayuki
CEPTITLE OF INVENTION: Programmed Cell Death Genes and Proteins
TITLE OF INVENTION: 95
NUMBER OF SEQUENCES: 95
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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US-08-368-704C-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 DE-----SDEVD 101
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APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
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ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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                              MOLECULE TYPE: peptide
                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                TELEFAX: (200, SK TELEX: 248636 SSK
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                                                                                                                                                                                                                                                                                                                                                                      NAME: Bugaisky, Lawrence B
REGISTRATION NUMBER: 35,080
                                                          STRANDEDNESS: unki
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                                                                                                                                               LENGTH:
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Similarity 35.6%;
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                                                                                                                          amino acid
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     418 amino acids
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4-JAN-1995
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                                                                                                        unknown
                                                                                                                                                                                                                                                                    371-2540
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US-08-368-704C-55
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                                                                                                                                                                                                                                                                                                          LENGTH: 419 amino acido
TYPE: amino acido
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
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APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                       82 EQLSLQFSNDEDD 94
                                                                                                                                    95 DE-----SDEVD 101
                                                                                                                                             26 VEDDLVEK----NYLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSO 81
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APPLICATION NUMBER: US
FILING DATE: 10-JUN-15
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                              Match 13.2%; Score 75.5; DB 3; Length 419; Local Similarity 35.6%; Pred. No. 3; Length 419; Les 26; Conservative 14; Mismatches 14; Indels 19
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371
TELEX: 248636 SSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bugaisky, Lawrence B. REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/080,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-MS-DOS
SOFTWARE: Patentin Release #1.0.
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1100 New York Avenue, Suite 600
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N: 435
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                                                                                                                                                                                                                RESULT 10
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                                                                                     Sequence 1, Application US/08170360
Patent No. 5656602
GENERAL INFORMATION:
APPLICANT: Tseng, Albert P. S.
APPLICANT: Inglis, Adam
TITLE OF INVENTION: PLA2 INHIBIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-368-704C-55
                                                                                                                                                                                                                                                                                                                                                                                    Matches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                       CORRESPONDENCE ADDRESS:
                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 08/080,850
APPLICATION DATA:
APPLICATION UNDER: US 08/080,850
APPLICATION DATE: 24-JUN-1993
             ADDRESSEE: Rothwell, Figg Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/08368704C Patent No. 6087160
                                                                                                                                                                                                                                                    82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BUGALSKY, LAWTENCE B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 060
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  95 DE-----SDEVD 101
                                                                                                                                                                                                                                                                                             26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
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Local Similarity 35.6%; Pred. No. 3;
nes 26; Conservative 14; Mismatches 14; Indels 19; Gaps
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NAME: Bugaisky, Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Programmed Cell Death Genes and Proteins CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/(FILING DATE: 4-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
Washington D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1993
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                                                                              PLA2 INHIBITORY COMPOUNDS
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Matches Query Match

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US-08-961-083-200
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                                                                                                                                                                                                                                                                                                                                                       Sequence 200, Application US/08961083 Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                               COMPUTER: HP Vectra 480
OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                             APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEO ID NO: 1:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)783-6040
                   FILING DATE:
                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: ERDSt, Barbara G.
REGISTRATION NUMBER: 30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: AU PO
FILING DATE: 06-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 LDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  38 VDELDRCCETHDNCY-------RDAKNLDSCKELVDNPYTESYSYSCSNTE 81
                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                               20850
                                                                                                                                                                                                                                        Rockville
                                                                                                                                                                                                                        Maryland
                                                                                                                                                                                                                                           9410 Key West Avenue
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                                                                                                                                                                                                                                                           Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                            MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%; Score 69.5; Di
27.1%; Pred. No. 2.9;
                                                                                    US/08/961,083
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                                                                                                                                                       3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches 20; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1871-104A
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US-08-170-360-2
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Patent No. 565602
GENERAL INFORMATION
APPLICANT: Tseng, Albert P. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: US-08-961-083-200
                                                                                                               APPLICATION NUMBER: AU PCT/AU92/PILOR DATE: 06-JUL-1992
PATOR APPLICATION DATA: AU PK 7058
APPLICATION NUMBER: AU PK 7058
FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: EINST, BALDAIA G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                         INFORMATION FOR SEQ ID NO
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MOLECULE TYPE:
                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                           STRANDEDNESS:
                TOPOLOGY:
                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0:
FILING DATE: 03-MAR-1994
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TOPOLOGY: lin
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REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                          amino acid
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                                                      124 amino acids
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                                                                                    (202)783-6031
(202)783-6031
(202)783-6031
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Suite 701-E, 555 Thirteenth St., N.W
          linear
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Inglis, Adam
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SYSTEM: PC-DOS/MS-DOS
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protein
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                           single
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23.6%; Pred. No. 23;
                                                                                                                                                                                                                                                                          AU PCT/AU92/00333
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                                                                                                                     , MOLECULE TYPE: protein US-08-888-497-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                     Query Match 11.7%; Score 67; DB 2; Length 124; Best Local Similarity 22.7%; Pred. No. 5.4; Matches 17; Conservative 14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
ANTI-SENSE:
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                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tischfield, Jay A.

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOTTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 DLDRC---CQTHDHCY------NQAKKLESCKFLIDNPYTNTYSYKC---- 77
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 200 East Brows
CITY: Fort Lauderdale
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/888,497
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                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/097,354 FILING DATE: 26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
  27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                     LENGTH:
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5972677
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                                                                                                                                                                                                    amino acid
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Seilhamer, Jeffrey J.
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22.7%;
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RESULT 14
US-09-362-230-41
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Patent No. 6352849
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RESULT 15
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                                                                                                                                                                                    Best Local Similarity 22.7 Matches 17; Conservative
                                                                                                                                                                                                                    Query Match
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INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-JUL-1993 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/362,230
                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                 40 DLDRC---CQTHDHCY------NQAKKLESCKFLIDNPYTNTYSYKC---- 77
                                                                                                                                                  27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                   SGNVITCSDKNNDCE 92
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Seilhamer, Jeffrey J.
                                                                                                                                                                                                                                                                                                                                        124 amino acids
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                                                                                                                                                                                                                                                                                          linear
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Sequences and Low Molecular Weight Amino Acid Sequences
Encoded Thereby, Antisense Sequences and Nucleotide
Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                      11.7%; Score 67; DB 4; Length 124; 22.7%; Pred. No. 5.4; tive 14; Mismatches 22; Indels
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PCT-US94-07926-41

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Search completed: February 25, 2003, 02:33:47 Job time : 16 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07926-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US94/07926

PILING DATE: 15-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION UMBER: US 08/097,354

FILING DATE: 26-JUL-1993

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,264

REFERENCE/DOCKET NUMBER: 1N21044-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: 305-572-2498

INFORMATION OF SECULARY SECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADDITICATION NUMBER: PCT/US94/07926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application PC/TUS9407926 GENERAL INFORMATION:
                                                                                                                                                                 78 SGNVITCSDKNNDCE 92
                                                                                                                                                                                                                                       87 AGNAAGTGDESDEVD 101
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                                                                                                                                                                                                                                                                      40 DLDRC---CQTHDHCY------NQAKKLESCKFLIDNPYTNTYSYKC---- 77
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APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammallan Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
11.7%; Score 67; DB 5; Length 124;
Local Similarity 22.7%; Pred. No. 5.4;
es 17; Conservative 14; Mismatches 22; Indels
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ZIP: 33301
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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seq length: 2000000000
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573
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               13.2
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                   Length
               1453
1962
1973
1998
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1167
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590
294
1387
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               US-09-974-298-114
US-09-925-297-511
2 US-10-042-417-52
2 US-10-092-219-8
US-09-930-871-18
US-09-930-871-18
US-09-930-871-20
US-09-930-871-20
US-09-930-871-6
US-09-930-871-6
US-09-930-871-16
US-09-930-871-16
US-09-930-871-14
US-09-930-871-14
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US-09-833-790-252

US-09-815-242-11522

US-09-765-272-200

US-09-933-999-7
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sequence 7, Appli
Sequence 51, Appl
Sequence 511, App
Sequence 512, Appl
Sequence 52, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 20, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
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Sequence 18, Appli
Sequence 2, Appli
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252, App
11522, A
200, App
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| 10.7<br>10.7<br>10.7<br>10.7<br>10.6<br>10.6<br>10.6<br>10.6  | 11.0<br>10.9<br>10.9<br>10.9<br>10.9<br>10.9<br>10.9<br>10.7<br>10.7   |
| 292<br>292<br>2012<br>2012<br>2437<br>6281<br>429<br>1686<br>467<br>976<br>1036<br>11036<br>1178<br>1178  | 2009<br>322<br>571<br>578<br>1168<br>1172<br>1172<br>1172<br>225<br>270<br>270   |
| 10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10  | 10<br>10<br>10<br>10<br>10<br>10<br>10<br>10   |
| US-09-745-763-166 US-09-862-027-14 US-09-886-602-68 US-09-815-242-5834 US-09-815-242-12996 US-09-815-242-10854 US-09-815-242-10854 US-10-092-219-2 US-09-916-384A-7 US-09-918-508-4 US-10-135-322-18 US-10-041-856-9 US-09-924-154-13   | US-09-930-871-12<br>US-09-872-523-3<br>US-09-872-523-3<br>US-09-925-301-1031<br>US-09-9821-839-2<br>US-09-919-603-2<br>US-09-919-770-4<br>US-09-867-550-2038<br>US-10-185-770-4<br>US-09-816-028A-39<br>US-10-125-852-23<br>US-10-125-852-23 |
| Sequence 16, Appl<br>Sequence 16, Appl<br>Sequence 68, Appl<br>Sequence 584, Appl<br>Sequence 584, Appl<br>Sequence 51296, A<br>Sequence 10854, A<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 18, Appli<br>Sequence 18, Appli<br>Sequence 18, Appli<br>Sequence 19, Appli<br>Sequence 19, Appli | e 12, e 2,   |

#### ALIGNMENTS

RESULT 1 US-09-989-903-16

Sequence 16, Application US/09989903 Patent No. US20020146804A1

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GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434D1
CURRENT APPLICATION UNMBER: US/09/989,903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 172
TYPE: PRT
ORGANISM: Mus musculus
US-09-989-903-16
                                                                                                                                                           RESULT 2
US-09-833-790-252
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                    Sequence 252, Application US/09833790
Patent No. US20020068288A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
      APPLICANT:
                                                                                                                                                                                                                                                  82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                         95 DE-----SDEVD 101
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                                                                                                                                                                                                                                                                                                                                   26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
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Mohamath, Raodon
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                  ; ORGANISM: Helicobacter pylori US-09-815-242-11522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-11522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 252
LENGTH: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11522, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                      Matches
                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11522
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER:
                                                                                                                                                             TYPE: PRT
                                                                                                                                                                           ENGTH:
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19 DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENY 78
                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYSRADAENAMRYINGTRIDDR--IIRTDWDAGFK---EGRQYGRGRSGGQVRDEYRQD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEQEKLLKKSCTLYVGNLSFYTTEEQIYELFSKSGDIKKIIMGLDKMKKTA--CGFCFVE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EERE-----DCWTFYANRKYTDFDKS----FKKSSD------LDECKKTCFKTEYCYIV 44
                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                             1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indirias, Carol Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert T.
Xu, H. Howard
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                         12.2%;
                                                                                                                                                                                                                                                                                                                  60/257,931
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                                        12;
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                                                         Score 70;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70.5; DI Pred. No. 2.1;
                                        Mismatches
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                                                                           10; Length 1167;
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                                        24;
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                                        Indels 18;
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                                        Gaps
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RESULT 4
US-09-765-272-200
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                                                                            US-09-993-999-7; Sequence 7, Application US/09993999; Patent No. US20020110891A1
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                                                                                                                                  RESULT 5
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Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
GENERAL INFORMATION:
APPLICANT: Ho, I-Cheng
APPLICANT: Arm, Jonatl
APPLICANT: Austen, K.
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                         322 WIKQLNKRLEKFD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 DKTEQSSNDPKEAQKTLFDA----ILLQDLAN--AVYNVMPTK-----LGDRNYWENF 286
                                                                                                                                                                                               369 QEDKALYLDCDLVVTKNLDDLFATDLQDYPLAAVRDFGGRAYFGQE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                   62 ELDQEKF-----VVDENFTENYLTDCEG-----KDAGNAAGTGDE 96
                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                           7 WIFYANRKYIDEDKSFKKSSDLDECKKI-----CFKTEYCYIVFEDTVNKECYYNVVDGE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 200:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTDCEGKDAGNAAGTGDE
                                                                                                                                                                                                                                                                                                                                                    l Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 674 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
    Arm, Jonathan P. Austen, K. Frank
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (301)
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23.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200:
                                                                                                                                                                                                                                                                                                                                                    17;
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                                                                                                                                                                                                                                                                                                                                                                      Score 69.5;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                      35;
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US-09-974-298-114
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                                                                                                                                     GENERAL INFORMATION:
  APPLICANT: Chen, Huel-Mel
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR APPLICATION NUMBER: 60/238,331
                                                                                                                                                    Sequence 114, Application US/09974298 Patent No. US20020156263A1
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; Sequence 57, A
PRIOR FILING DATE: 2000-05-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Reproduction-Specific Genes FILE REFERENCE: 0399.2007-002
CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 90
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                                                                                                                                                                                                                                                              1400 NE-----TNVTENYELDV-----ASGTEED 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Peijing Jeremy APPLICANT: Page, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                              1349 SSKSYLDKORILTVDSFAASSTVPHCEQSCREKELLKTEQC-----SSGNCLH--TDG 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2789
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CURRENT FILING DATE: 2001-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glimcher, Laurie H.
TITLE OF INVENTION: Phospholipase A2 Group Preferentially
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REFERENCE: HUI-046
                                                                                                                                                                                                                                                                                                  61 EELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDE 96
                                                                                                                                                                                                                                                                                                                                                                      11 ANRKYTDFDK-----SFKKSSDLDECKKTC----FKTEYCYIVFEDTVNKECYYNVVDG 60
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 DLDECKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              h 11.6%; Score 66.5; DB 10; Length 2789; Similarity 26.0%; Pred. No. 1.5e+02; 25; Conservative 13; Mismatches 23; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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                                                                                                                                                                                                                                                                                                                                                                                                            Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Gaps
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RESULT 9
US-10-042-417-52
Sequence 52, Ap
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US-09-925-297-511
; Sequence 511, Application US/09925297
; Patent No. US20020081659A1
                                                                                                                                                                                         Sequence 52, Application US/10042417 Patent No. US20020123082A1
                    GENERAL INFORMATION:

APPLICANT: Pagano, M.

TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF

TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REFERENCE: 5914-090-999

CURRENT APPLICATION NUMBER: US/10/042,417

PRIOR APPLICATION NUMBER: 5002-01-07

PRIOR APPLICATION NUMBER: 60/260,179

PRIOR FILING DATE: 2001-01-5

PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
LOCATION: (156)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US00/05989 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,297 CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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SOFTWARE: PERL Program
SEQ ID NO 114
LENGTH: 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                       68 VDELDKCCQTHDNCY----DQAKK------LDSCKELLDNPYTHTYSYSCSG 109
                                                                                                                                                                                                                                                                                                                                 28 LDECKKTCFKTEYCYIVFEDTYNKECYYNVYDGEELDQEKFYVDENFTENYLTDCEG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1076 EEVEEAENEGEEAKTEGLMKDDRAESQASSLGQKVGESSEQVSEE 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Incyte ID No. US20020156263A1 3267030CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032 EEDED-----SEKEEEEEDKEMEELQEEKECEKPOGDEE-----EEEEEEE-----VEE 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EELDQEKFVVDENFTENYLTDCEGKDAGNAAG--TGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 64.5; DB 10; Length 156; 29.8%; Pred. No. 8.8; ative 5; Mismatches 20; Indels 15.
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ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: SITE
LOCATION: all Xaa positions
OTHER INFORMATION: Xaa-unknown amino acid residue
US-10-042-417-52
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SEQ ID NO 52
LENGTH: 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/092,219
CURRENT FILING DATE: 2002-03-07
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: PCT/GB98/00244
PRIOR APPLICATION NUMBER: 09/355,160
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 9701652.1
PRIOR FILING DATE: 1997-01-28
PRIOR FILING DATE: 1997-01-28
PRIOR FILING DATE: 1997-01-28
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Patent No. US20020115114A1
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                                                                                                                       Sequence 8, Application US/09930871
Patent No. US20020076780A1
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                       APPLICANT: Mathur, Daniel APPLICANT: Mathur, Brian APPLICANT: Mathur, Brian APPLICANT: Mathur, Brian TITLE OF INVENTION: NO. US20020076780Alel Human Ion Channel Proteins and Polynucleoti TITLE OF INVENTION: Same 5 TITLE OF INVENTION: Same 5 TITLE OF INVENTION: Same 5 TITLE REFERENCE: LEX-0216-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 TSHQSGFLKTS-TSKITSTAWKNK--DITMQSTKQYACLHDLTNKGIGEEIDNEHPWTKP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 VSSENFTSPYVWMLDAEDLADIEDT 337
CURRENT APPLICATION NUMBER: US/09/930,871
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                                                                                                                                                                                                                                                                                                      104 LLDDNF 109
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                                                                                                                                                                                                                                                                                                                                                                                                                              12 NRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ---EKF 68
                                                                                                                                                                                                                                                                                                                                              69 VVDENF 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
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Similarity 28.8%; Pred. No. 26;
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US-09-930-871-8
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US-09-930-871-10
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LENGTH: 1381
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PRIOR APPLICATION NUMBER: US 60/225,989
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 20
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RESULT 13
US-09-930-871-18
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OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/930,871
CURRENT FILING DATE: 2001-08-14
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: US 60/225,989
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mathur, Brian TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucle TITLE OF INVENTION: Same
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                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(1387)
OTHER INFORMATION: Xaa = Any Amino Acid
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                                                                               1063 D-----YLKDVNGTTSGIGTGSSVEKYIIDE 1088
                                                                                                                                                            1014 YVKRKIYEFIQOSFIRKOKILDEIKP------LDDLNNKKDSCMSNHTXEIGKDL 1062
                                                                                                                                                                                                   10 YANRKYTDF-DKSF-KKSSDLDECKKTCFKTEYCYIVFEDTVNKE--CYYNVVD--GEEL 63
                                                                                                                     64 DQEKEVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDE 102
                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                   11.0%; Score 63; DB 10; Length 1387; 28.3%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                        10; Mismatches
                                                                                                                                                                                                                                                                 31; Indels 30; Gaps
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; Sequence 18, Application US/09930871; Patent No. US20020076780A1; GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/930,871
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,989
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FRStSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 1398
TYPE: PRT
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; NAME/KEY: VARIANT
; LOCATION: (1)...(1392)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-930-871-18
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; LOCATION: (1)...(1398)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-930-871-20
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Best Local :
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LENGTH: 1392
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/930,871
CURRENT FILING DATE: 2001-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Daniel
APPLICANT: Mathur, Brian
TITLE OF INVENTION: No. US20020076780Alel Human
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/225,989
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 20
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1074 D-----YLKDVNGTTSGIGTGSSVEKYIIDE 1099
                                                                             1025 YVKRKIYEFIQQSFIRKQKILDEIKP----
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                                      64 DQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDE 102
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                                                                                                                   YANRKYTDF-DKSF-KKSSDLDECKKTCFKTEYCYIVFEDTVNKE--CYYNVVD--GEEL
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28; Conserv
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Mathur, Brian
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                                                                                                                                                            11.0%; Score 63; DB 10; I
28.3%; Pred. No. 1.5e+02;
ative 10; Mismatches 31;
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Pred. No. 1.5e+02;
0; Mismatches 31;
                                                                               ---LDDLNNKKDSCMSNHTXEIGKDL 1073
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                                                                                                                                                                                                   Length 1398;
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; LOCATION: (1)...(1442)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-930-871-6
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Search completed: February 25, 2003, 02:34:14
Job time : 13 secs
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                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                 Query Match
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TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucle
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: LEX-0216-USA
CURRENT APPLICATION NUMBER: US/09/930,871
CURRENT FILING DATE: 2001-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mathur, Daniel APPLICANT: Mathur, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/225,989 PRIOR FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Turner, C. Alexander Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1442
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapiens
                                                                                   1063
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                                                                                                                             64 DQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDE 102
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28.3%;
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Pred. No. 1.6e+02;
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-Q-/cgn2_1/USPTO_spool/US09936737/runat_14022003_100732_2291/app_guery.fasta_1.263
-Q-/cgn2_1/USPTO_spool/US09936737/runat_16020001_-LOOPCL=0 -LOOPEXT=0
-DB=Cenembl -OgwT=fastap -SUFFIX=rge -MINNATCH=0.1 -LOOPCL=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -THR_MAX=1100 -THR_MIN=1100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=1100 -THR_MIN=00000000
-UUTEMT=pto -NOAM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09936737_@CGN_1_1_2425_@runat_14022003_100732_2291 -NCPU=6 -ICPU=3
-US_NUMBER-US09936737_@CGN_1_1_2425_@RUNATUS097=10 -NCARPEXT=7
-NO_NUMBER-US09936737_WARPUS097=120
-NO_NUMBER-US099367_WARP
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36: em_htg_vrt:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_other:*
40: em_htgo_other:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 8011   | AC007305      | AC012139           | AC111055           | CEHOTO 1              | BKG4/C             |               | 058/62        |            | ū    | TRBCARM1 | AC006281      | AL445568 | AB019231  | PFMAL13P3 | AP001517 | AC006889           | AL356116 | PFMAL3P2       | HSGEND | AC024847 | AP003192 | AL663030 | CEF40G12  | CELEOUER<br>CEN131985 | ACTOSO / O  | ACT08477_4 |        | PEDNACPT   | AR030964 | SFU15038 | AC115173 | 0           |       | ם מ        | 0 1   | 1281               | FMAI.1302 2 | 1120      | av036541          | ID               |
| ARIU2119 Sequence ARIU3163 Sequence BC028979 Mus muscu | 7305 Mus musc | ACO12139 Homo sapi | AC111055 Mus muscu | z98852 Caenorhabdi    | Z68135 Caenorhabdi | 4663 Caenorha | 549 Restrepia | Caenorhabo | 2    | 100      | TACINOTAL TRA |          | 231 ALGOL | 04        |          | ACUU6889 Caenornan | 0 1      | 34558 Plasmout | 4346 H | 4847     | 003192   | w        | Caenorhal | ū                     | 478 Caenorl | Rattus     | uat    | 500 Rattus | ă C      | ds       | 5173     | 1018 Rattus | 83    | m          | 09947 | AC131381 Strongylo | inuation (3 | ontinuati | AX036541 Sequence | Description      |

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          Sequence split into 4 fragments LOCUS PFMAL13P2 Accession AL049185 Fragment Name Begin End
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                                                                                                                                                                                                                                                                                                                                                                             Protein for blocking platelet adhesion Patent: WO 0056885-A 1 28-SEP-2000;
HEMBERGER JUERGEN (DE) ; MERCK PATENT GMBH (DE) ; SCHEUBLE BERNHAI (DE) ; STRITTMATTER WOLFGAMG (DE) ; HOFMANN UWE (DE) ; FOTEV ZISI (DE) ; GUESSOW DETLEF (DE)
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1 (bases 1 to 375)
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/protein_id="cac16481.1"
/db_xref="GI:11256152"
/translation="EDREDCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1257 GTTCTAAATCAAACTTCAAAAAAAAAATAATTTAGATTTTGATAATCATGATGTGGAGCAA 1198
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1 (bases 1 to 138024)

Davidson,E.H., Rast,J.P., Oliveri,P., Ransick,A., Calestani,C., Yuh,C.-H., Minokawa,T., Amore,G., Hinman,V., Arenas-Mena,C., Otim,O., Brown,C.Titus., Livi,C.B., Lee,P.Y., Revilla,R., Schilstra,M.J., Clarke,P.J.C., Rust,A.G., Pan,Z., Arnone,M.I., Rowen,L., Cameron,R.Andrew., Meyal,D.R., Hood,L. and Bolouri,H A provisional regulatory gene network for specification of endomesoderm in the sea urchin embryo Dev. Biol. 246 (1), 162-190 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-AUG-2002) Multimegabase Sequencing Center, Institute for Systems Biology, 1441 N. 34th Street, Seattle, WA 98103, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinoida;
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AC131381.1 GI:22380705
HTGS_PHASE2; HTGS_FULLTOP.
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Strongylocentrotus purpuratus clone
PROGRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that he provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 138024)
                                                                                                                                                                                 Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-trimer Big Dye; 10% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                             Drafting center: ISBMSC
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                          Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Multimegabase Sequencing Center
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                             between them are based on estimates that have
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Best Local Similarity:
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||||||:::|||:::||||||
On Apr 30, 2001 this sequence version replaced gi:13751877. On Apr 30, 2001 this sequence version replaced gi:13751877. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 58994 contig of 58994 bp in length

* 58995 59094 gap of unknown length

* 59095 96228 contig of 37134 bp in length

* 96229 96328 gap of unknown length

* 96329 138024 contig of 41696 bp in length.
                                                                                                                                                                                                                                                                    Submitted (11-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete sequence. AL109947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                              requests: clonerequest@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                        Johnson,C.
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/note="This library is described in Cameron, R.A.,
Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, J., Livingston
, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J,
Davidson, E.H., Hood, L. Proc. Natl. Acad. Sci. U.S.A. 97
(17): 9514-8 2000"
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/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
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52.83%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of clone RP5-919F19 The true left end of clone RP5-1036D8 is at 86977 in this sequence. The right end of clone RP11-425D10 is at 56374 in this sequence.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/HGP/Chr6
RP5-919F19 is from the library RPCI-5 constructed by the group
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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/note="AluSg re
12339. 13410
/note="LIMA2 re
13633. 13852
                                                                                                                                                                                                    consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                 6393. .6686 /note="Alux repeat: matches 1. .301 of consensus" 6998. .7112
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/note="LIMC/D repeat: matches 5276.6393. .6686
                                                                                                                                                                                                                                                                                /note="LIMA2 repeat: matches 4193. .4614 of consensus" 9339. .11100
                                                                                                                      /note="%LRAS2 repeat: matches 1..392 of consensus"
11510..12032
/note="%LRAS2 repeat: matches 4604..5114 of consens
                                                                                                                                                                                                                                                                                                                                                                                    3372. .8434
/note="L1MA2 repeat: matches 4133. .4193 of consensus"
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/note="L1MC5 repeat: matches 6834. .7364 of consensus"
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/note="AluSx repeat: matches 1.
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/chromosome="6"
                                                                                                                                                                                                                                                      /note="MER66-internal repeat: matches 4895. .6676 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1512. .4698
/note="IIMC5 repeat: matches 7347. .7537 of consensus"
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"note="Alusg repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             map="q16.3-22.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RP5-919F19"
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te="AluJo repeat: matches l. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5. .2424
te="FLAM_A repeat: matches 1. .123 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="FLAM_A repeat: matches l. .115 of consensus"
                          repeat: matches 5114.
                                                                         repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 505. .914 of consensus"
                                                                                                                           matches 4604. .5114 of consensus
                                                                                                                                                                                                                                                                                                                                                       matches 1.
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                            .6307 of consensus'
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/note="TIGGER2 repeat: matches 863. .1266 of consensus"
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13896. .15355
/note="MIGGER2 repeat: matches 1266.
15356. .15657
/note="AluJb repeat: matches 1.
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                                         /note="AluSc repeat: matches 1.
                                                                              note="20 copies 2 mer tg 87% conserved"
                                                                                                                                                            /note="MER81 repeat: matches 3.
                                                                                                                                                                                                                                                                             31786. .31914
/note="FLAM_C repeat:
                                                                                                                                                                                                                                                                                                                                                         note-"LTR23 repeat: matches 204. .437 of consensus"
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24622. .24927
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/note="AluSq repeat: matches 1.
l9209. .19517
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29588. .29879
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                                                                                   DEFINITION
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Best Local Similarity:
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                                                                                                                                                                                         88 GlyAsnAlaAlaGlyThrGlyAspGluSerAspGluValAsp 101
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                                                                                                                                                                                                                                                  PheValValAspGluAsnPheThrGluAsnTyrLeuThrAspCysGluGlyLysAspAla 87
                                                                                                                                                                                                                                                                                     LysLysSerSerAspLeuAspGluCysLysLysThrCysPheLys-----ThrGluTyr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt ArgGluAspCysTrpThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPhe}
                anti-platelet
 anti-platelet protein. Haementeria officinalis cDNA to mRNA.
                                    M81489.1 GI:159220
                                                                                 Haementeria
                                                                                                  HEILAPP
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39348..40556
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/note="L2 repeat: matches 2622. .2690 of consensus"
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US-09-936-737A-2 (1-103) x HEILAPP (1-563)
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                                                                                                                                                                                                                                                                                                                        CysTyrIleValPheGluAspThrValAsnLysGluCysTyrTyrAsn 56
                                                                                                                                                                                                                                                                                                                                                                      GAATTCACCAGCGTCGATGAATGCAGAAAGATGTGCGAAGAATCTGCCGTGGAACCATCC 369
                                                                                                                                                                                                                                                                                         TGCTACATTCTGCAAATCAACACAGAAACCAACGAATGCTATAGAAAT 417
                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haementeria officinalis Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Rhynchobdellida; Glossiphoniidae; Haementeria.

1 (bases 1 to 563)
Keller, P.M., Schultz, L.D., Condra, C., Karczewski, J. and
                                                                                                                                                                                            Human DNA sequence from
Lloyd
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J. Biol. Chem. 267 (10), 6899-6904 (1992)
92202247
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/gene="LAPP"
/product="anti-platelet protein"
563
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TPSTGGGGDGGNEETITAGNEDCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVE
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58. .501
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/product_"anti.platelet protein"
/protein_id="AAA29194.1"
/db_xref="GI:159221"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP11-554F20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-554F20 is at 1 in this sequence. The true left end of clone RP11-30L7 is at 95516 in this sequence. The true right end of clone RP11-547C13 is at 37658 in this
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/note="5 copies 9 mer tgtctggtg 88% conserved"
                                                                                                                                       6248. .6480
/note="L2 r
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/note="AluJo repeat: matches 7.
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/db_xref="taxon:9606"
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/note="L2 repeat: matches 2009. .2207 of consensus"
/note="MIR repeat: matches 8.
                                                                   'note="AluJb repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MIR repeat: matches 61. .207 of consensus"
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                                                                                                                                                                                                           note="MER96 repeat: matches 91. .174 of consensus"
                                                                                                                                                                                                                                                                                   'note="MIR repeat: matches 123.
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                                                                                                                                       repeat: matches 1988. .2234 of consensus"
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       of.
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20734. 20950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: 9586. .9894
                                                                                                                                                                                                           /note="Tigger3(Golem) repeat: matches 2276. .3028 of
consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 124. .245 of consensus"
26655. .26892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2646. .2708 of consensus"
10421. .10489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 16. .190 of consensus"
13382. .13680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2348.
                                                                                                           /note="29 copies 2 mer at 70% conserved"
29188. .29307
                                                                                                                                                                                                                                                                                      /note="Tigger3(Golem)
28394. .29077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 1. .253 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2459. .2747 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1MA8 repeat: matches 5660. .6286 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 29. .235 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 68. .132 of consensus"
24151. .24345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 47. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 13. .163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1MB5 repeat: matches 5777. .6165 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER46C repeat: matches 118. .319 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 2177. .2418 of consensus"
L7533. .17662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L2 repeat: matches 2656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT1D repeat: matches 411. .495 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"MLT1D repeat: matches 143. .457 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="L2 repeat: matches 2231.
       note="MIR repeat: matches 51. .112 of consensus"
                                                                           /note="L2 repeat: matches 2625.
                                                                                                                                                                                                                                                                                                                                                              /note="AluSq repeat: matches 1.
28301. .28417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 6. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="MIR repeat: matches 10. .250 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MLT1A1 repeat: matches 1. .365 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"L2 repeat: matches 2613. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="MER1A repeat: matches 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="MIR repeat: matches 20. .111 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .9531
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                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 1815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I repeat: matches 65. .410 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 2180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 48. .118 of consensus*
                                                                                                                                                                                                                                                                                                                      repeat: matches 1. .122 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                              .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .260 of consensus"
                                                                              .2748 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2289 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2747 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2738 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2299 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2419 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .527 of consensus"
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AC101018
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              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                      95475 GAGCACTGTAAAAAGAGTAGGTTTGTAGTGGAGGAA 95510
                                                                                                                                                                                                                                                                                                                                         95304 GAGCCATGTAGGGGGTAAGAGGCAGCCAGATCCTATATAGATTTTGAAAAAGCA----- 95357
                                                                                                                                                                                                                                                          95415 TGTCACCAAAATTTTTGGCCCTGGAAACTGAAAGAACAGAGTTATCATGTGCTGAAAGGG 95471
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                                                                                                                                          61 GluGluLeuAspGlnGluLysPheValValAspGlu 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No . :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                  41 CysTyrIleValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGly 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
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                                                                                                                                                                                                                                                                                                 24 LysSerSerAspLeuAspGluCysLysLysThrCysPheLysThrGluTyr----- 40
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                                                                                                                                                                                                                                                                                                                                                                           4 GluAspCysTrpThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLys 23
      AC101018 149109 bp 1
Rattus norvegicus clone RP32-328P7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MSTA repeat: matches 200. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MSTA repeat: matches 1. .229 of consensus" 44088. .44127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Tigger4(Zombi) repeat: matches 3. .124 of consensus" 43860. .44067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 95. .252 of consensus" 42788. .42921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 81. .180 of consensus" 37170. .37243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1MA9 repeat: matches 5693. .5786 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 2555. .2691 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluYb8 repeat: matches 1. .318 of consensus"
41844. .42158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40985.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="28 copies 2 mer tt 73% conserved"
13604. .43697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="16 copies 2 mer ga 84% conserved"
40985. .41325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 21. .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="12 repeat: matches 2153. .2750 of consensus"
38695. .38938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 77. .148 of consensus" 37581. .38098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER5A repeat: matches 3. .110 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2626. .2702 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIT1B repeat: matches 7. .390 of consensus" 33200. .33272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluY repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.618
36.118
14.498
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DNA linear HTG 21-AUG-2002
, *** SEQUENCING IN PROGRESS ***,
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Center project name: L1479 Center clone name: 328\_P\_7

Contact: sequence\_submissions@genome.wi.mit.edu

Web site: http://www-seq.wi.mit.edu

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                                                                                                                                                                                                                                                                                                                                                                          CE 3 (bases 1 to 149109)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farror, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS Birren, B. Linton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Gamarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Junes, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCean, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Myuyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stange, Theman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Tresfaye, S., Theodore, J., Vlel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., alinoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                            Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17059792. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus, clone RP32-328P7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC101018.2 GI:22381320
Center code: WIBR
                          Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                           Genome Center
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                     KEYWORDS
                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                      AC115173/c
                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61509 GACTACTTGTATGTCGACGAGGAAGAAGAGGTGGAGGACGACATCTACTATGACAGTTAC 61568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61569 ---TATTACAAATACGAAGATGAAAACATCTACGAAGATGAAAACATCTACTATGATAAC 61625
                                                                                                                                                                                                                                                                                                                               61686 GACGATGTCGACGACGAC 61703
                                                                                                                                                                                                                                                                                                                                                                                                                               61626 TATGATGTTGACAATGACAATGACGATATTGACAATTACGATAACGACGACGACGATGAT 61685
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No::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 TyrLeuThrAspCysGluGlyLysAspAlaGlyAsnAlaAlaGlyThrGlyAspGluSer 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AspGlyGluGluLeuAspGlnGluLysPheValValAspGluAsn---PheThrGluAsn 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 GluTyrCysTyrIleValPheGluAspThrValAsnLysGluCysTyrTyrAsnValVal 58
                                                                                                                                                                                                                                                                                                                                                                                98 AspGluValAspGluAsp 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                  Rattus norvegicus clone CH230-286017, *** SEQUENCING IN PROGRESS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                      Rattus norvegicus
                                                                                                                                                      AC115173
                                                                                                                                                                                                                               AC115173
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                                                                                                       HTG; HTGS_PHASE1.
                                                                                                                               AC115173.2 GI:21738030
                                                                                                                                                                             ***, 46 unordered pieces.
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77197 77296; gap of 100 bp
77197 77296 gap of 100 bp
77297 99453; contig of 22157 bp in length
99454 99553; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102880 102979: gap of 100 bp 102880 120352: contig of 17373 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131547 131646: gap of 
131647 149109: cont
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120453 131546: contig of 11094 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49622 49721: gap of 100 bp
49722 70009: contig of 20288 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46830 46929:
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34316 c 35185 g 39719 t 85
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/db_xref="taxon:10116"
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30.30%
14.49%
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929: gap of 100 bp
49621: contig of 2692 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ap of 100 bp
contig of 17463 bp in length.
                                                                                                                                                                                                                                 159492 bp
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REFERENCE
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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J.,
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Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabisi, A., Gao, J., Garcia, A., Ford, J., Hale, S., Hamilton, K.,
Garris, C., Harris, K., Hart, M., Havlak, P., Hale, S., Hamilton, K.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Holyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karatovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Kratovic, J., Lichtarge, O., Jieu, C., Liu, J., Liu, W., Loulseged, H.,
Li, J., Li, L., Lichtarge, O., Jieu, C., Liu, J., Liu, W., Loulseged, H.,
Lid, J., Liu, K., Mapua, P., Martin, R., Mandor, M., Martinez, E.,
Mansey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Norview, N., Newtson, J., Newtson, N., Nguyen, N.,
Norview, N., Nguyen, N., Nguyen, N.,
Norview, N., Nguyen, N., Nguyen, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:19482237.
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 124398 bases at least Q40 Consensus quality: 128059 bases at least Q30 Consensus quality: 131015 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                             Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                Center project name: GQDN Center clone name: CH230-286017
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Spodoptera frugiperda
                                      FK506 binding protein; immunophilin; peptidylprolyl cis-trans
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114404: gap of unknown length
122112: contig of 7708 bp in length
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Alnemri, E.S., Fernandes-Alnemri, T., Pomerenke, K., Robertson, N.M.,
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Alnemri,E.S., Fernandes-Alnemri,T. and Litwack,G.
Nucleotides encoding immunophilin FKBP46 and fragments thereof
Patent: US 5861498-A 1 19-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     31 ------CysLysLysThrCysPheLysThrGluTyrCysTyrIleValPheGluAsp 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 LysTyrThrAspPheAspLysSerPheLysLysSerSerAspLeuAspGlu----- 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JAN-1995) H.J. Yeo, CNRS URA 1856, Universite Montpellier II, Case 107, Place Eugene Bataillon, 34095 Montpellier, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeo,H.J
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                                                                                                                                                                                                                                                                                                                                                       Baylor Plaza,
On Jul 11, 20
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Web site: http://www.hgsc.bcm.tmc.edu/
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NOTE: Estimated insert size may differ from sequence length (see http://www.lgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
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34461 36532 36632 38636 38736

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Continuation (3 of 4) of AC108277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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WPCOMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24586 TACTGCTTTCTGGTATTCCAGCCAACC 24560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence split into 4 fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24646 ACTCGGTCAAGTGAGCTAAAGTATTAGGACTCTTGTCCAAAGCCCTCTGCTAAAACTTCT 24587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24706 CAGCCCTGTGTGGTTCCACGAATCACCGCCTACTCTAACTTTATGAAGAAACTGAAGTTG 24647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24766 AGAGGAGAGAATTGGGTATTTGTTGCTCATTCCGTCTTCCAGTTTTAGTTGGGTCAGATG 24707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37525 GATGTTTTGAATAAGAATGCTTTTTTAATACAATCTAGGGA 37484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37552 ---CTGGAAGAACCAAAGAGCACA-----TATTGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC108277_0
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AC108277_2
AC108277_3
RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankeaburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Ceveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Elagg, N., Ford, J., Foster, P., Frantz, P., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 TyrCysTyrIleValPheGluAspThr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragment Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ---LysSerSerAspLeu------AspGluCysLysLysThrCysPheLysThrGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 ----- ArgLysTyrThrAspPheAspLysSerPheLys--- 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 AspThrValAsnLysGluCysTyrTyrAsnValValAspGly 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ArgGluAspCysTrpThrPheTyrAlaAsn------
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC103570 232370 bp DNA linear HTG 12-JUL-2002 Rattus norvegicus clone CH230-10M24, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC103570.7 GI:21728494
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                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110000
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Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Lewis, L.C., Lewis, L.C., Lewis, L.C., Lewis, L.C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Maheshwari, M., Mener, Z., Mitchell, T., Mohabbat, K., Morgan, M., Mouris, S., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Mouris, S., Nguyen, N., Nickerson, E., Newtson, N., Nguyen, A., Nguyen, N., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Steney, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 38 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced g1:20467456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley,K.C
                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                       be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 196541 bases at least Q40
Consensus quality: 199662 bases at least Q30
Consensus quality: 201786 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 232370)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GDRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM
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1403: contig of 1403 bp in length 1503: gap of unknown length 2753: contig of 1250 bp in length 4531: contig of 1678 bp in length 4631: gap of unknown length 4631: gap of unknown length 5823: contig of 1192 bp in length 5923: gap of unknown length
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REFERENCE AUTHORS

TITLE JOURNAL

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AUTHORS JOURNAL

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COMMENT

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BASE COUNT
                                                                                                 FEATURES
source
     60783 a
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a 51173 c 49242 g 60940 t 10232 others
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129309: gap of unknown length
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139534: gap of unknown length
139534: gap of unknown length
154743: contig of 15209 bp in length
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166821: contig of 11978 bp in length
166921: gap of unknown length
186938: contig of 19817 bp in length
186838: gap of unknown length
207088: contig of 20250 bp in length
207088: gap of unknown length
207188: gap of unknown length
207189: gap of unknown length
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ig of 1474
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g of 1153
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g of 1122
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of 1065
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of 1268
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of 1778
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of 3074
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of 3704
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of 1421
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g of 2951
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of 3991
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of 7162
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of 5484
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of 9734 bp in length
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of 8710 bp in length
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| Alignment Scores:  Pred. No.:  Score:  Scorest Similarity:  Percent Similarity:  Best Local Similarity:  Oy  ArgCluAspCysTrpThrPheTyrAlaAsn |
|---|
| 12<br>ATG 93941<br>23<br>TTG 93881<br>Glu 39<br>TCT 93821   |
|   |

Search completed: February 25, 2003, 03:23:40 Job time: 2709 secs

```
Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-O_cgn2_1/USPTO_spool/US09936737/runat_14022003_100732_2281/app_query.fasta_1.263
-DB-N_Geneseq_101002 -OFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPCXT=0 -UNITS-bits -START=1 -END-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTPMT-pto -NORM-ext -HEARSIZE=500 -MINLEN-0 -MAXLEN-2000000000
-MODE-LOCAL -OUTPMT-pto -NORM-ext -HEARSIZE=500 -MINLEN-0 -MAXLEN-2000000000
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT-30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - nucleic search, using frame_plus_p2n model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                       18:
19:
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1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

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| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999, DAT: *
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA20010, DAT: *
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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|---|--|--|--|------------|
| 38<br>39<br>44<br>44<br>43  | 33<br>33<br>33<br>33<br>33<br>33<br>33<br>33<br>33<br>34<br>34<br>35   | 222222222222222222222222222222222222222  | 1 1 2 3 3 3 4 4 4 4 4 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6  | ult        |
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| 540<br>2010<br>2010<br>2095<br>3504<br>4994<br>344  | 1106<br>1261<br>1495<br>1826<br>1826<br>2155561<br>2299<br>9842<br>572<br>661<br>1187<br>1370  | 762<br>789<br>797<br>797<br>963<br>1092  | Length 375 2284 441 1107 587 587 7496 1399 1402 1402 1402 1402 1402 1402 1402 1403 2140 21403 21403 21403 21465 27684  |            |
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| AAV88360<br>ABL56367<br>ABL56450<br>ABL02089<br>AAS53788<br>ABL02988<br>ABL02988<br>ABL02988<br>AAS39459<br>AAK88317  | AAC37864<br>ABC68909<br>ABC70444<br>AAH17523<br>ABN71527<br>ABL22190<br>AAX20259<br>AAX20259<br>AAH81808<br>ABL62641<br>ABL30275<br>ABV25121 | ABN/0859<br>ABN68798<br>ABQ43620<br>ABQ43621<br>AAA70197<br>AAS55809                           | ID  AAA28180  AAX04441  AAQ23692  ABL26101  ABQ47469  ABQ47469  AAX20297  AAQ79969  AAX20297  AAQ79669  AAX731554  AAA77843  AAA77845  AAA77845  AAA7845  AAA7845  AAA7845  AAA78466  ABL20198  AAK84456  ABL20198  AAK77781   | SUMMARIES  |
| Human prostate exp EST clone DD12. H Nucleotide sequenc Nucleotide sequenc Drosophila melanog Helicobacter pylor Drosophila melanog CDNA encoding nove Human digestive sy | dopsis the ria monocy rola monocy rola monocy cDNA sequence phila mela burged different adenocars phila mela prostate prostate               | Streptococcus poly Streptococcus poly Oligonucleotide fo Plasmodium falcipa Streptococcus pneu | Platelet binding i S. frugiperda immu Leech antiplatelet Drosophila melanog Oligonucleotide fo Oligonucleotide fo Borrelia burgdorfe Human interleukin-Ich-3 cDNA. Mus S Murine caspase-12 Mouse Ice-4 coding Drosophila melanog Human immune/haema Drosophila melanog Drosophila melan |            |

## RESULT 1 AAA.28180 ID AAA.28180 standard; cDNA; 375 BP. XX AC AAA.28180; XX DT 29-JAN-2001 (first entry) XX DE Platelet binding inhibitor protein Saratin encoding cDNA sequence. XX KW collagen-dependent platelet adhesion inhibition; XX KW posterior capsule opacification; ss. CS Hirudo medicinalis. XX FH Key Location/Qualifiers 64..375

ALIGNMENTS

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for coating artificial surfaces, since use of Saratin renders them

CC non-adhesive for cells and prevents the activation of cells. It may also

CC be used for coating natural collagen surfaces. Furthermore, Saratin is

CC useful for modifying intraocular lenses in order to lessen the

CC thrombogeneatty of the lens material, for contacting the lens surface, or

CC is used for refractive anterior or posterior chamber ocular implants,

CC which may be implanted into the eye. This new type of coating avoids

CC medicaments that are for instance conferring cell death, Saratin coating

CC entibody immunospecific for Saratin, as well as Saratin itself, are

CC useful for measuring samples derived from host cell cultures or from a

CC creating metrin cortain
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                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Saratin polypeptide and gene isolated from Hirudo medicinalis for blocking platelet adhesion, especially useful for treating or preventing thrombotic diseases, or for manufacturing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-2000; 2000WO-EP02117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding Saratin, an expression vector comprising the DNA sequence, a host cell transformed with the expression vector, antibodies immunospecific for Saratin, and methods for identifying Saratin agonists or antagonists. Saratin is useful for treating thromboembolic processes, and for manufacturing a medicament for treating thromboembolic diseases. It is useful for preventing thrombotic diseases. Saratin is also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saratin is a protein isolated from the saliva of the medicinal leech Hirudo medicinalis. Saratin is an inhibitor of collagen-dependent platelet adhesion. The invention includes polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 40; 46pp; English.
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12-MAY-1999;
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124 TCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTAC
                  21 SerPheLysLysSerSerAspLeuAspGluCysLysLysThrCysPheLysThrGluTyr 40
                                                                 64 GAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACACACTTCGATAAA
                                                                                    1 GluGluArgGluAspCysTrpThrPhcTyrAlaAsnArgLysTyrThrAspPhcAspLys 20
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99EP-0109503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spodoptera frugiperda.
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This sequence represents the cDNA encoding the immunophilin FKBP46 from the moth Spodoptera frugiperda. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that bind to it. Such immunosuppressive agents can be used in treating transplant and tissue graft patients.
                                                                                 Isolated immunophilin FKBP46 nucleic acids - useful for developing products for the study and identification of immunosuppressive agents for treating e.g. transplant and tissue graft patients
                                                                                                                                         WPI; 1999-130433/11.
                                                                                                                                                            Alnemri ES,
                                                                                                                                                                                                              01-NOV-1995;
                                                                                                                                                                                                                                 31-OCT-1996;
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                                                              Claim 2; Fig 1; 21pp; English.
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                                                                                                                                                           Fernandes-Alnemri T,
                                                                                                                                                                                JEFFERSON THOMAS
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RESULT 3
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                                  WPI; 1992-125288/16
                                                                                      Connolly TN, Keller PM;
                                                                                                                                              (MERI ) MERCK & CO INC.
                                                                                                                                                                                                            09-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGAAC----ACATCAGCTGAAGGAGGATGACAGTGATGAAGAGGATGATGAAGA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TTCCTTGACGGTGAAGATATAGACACTGATGAA-----AATGATGAATCATTCAA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rAsnValValAspGlyGluGluLeuAspGlnGluLysPheValValAspGluAsnPheTh 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 803 A;
                                                                                                                                                                                                            90US-0594917
                                                                                                                                                                                                                                                                      91EP-0309157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64..441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= mature_LAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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81.50
43.12%
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14.22%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------GAAGACCAGCTTCAAAAG------ 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
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RESULT 4
ABL26101
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Best Local Similarity:
QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein to inhibit collagen simulated platelet aggregation extracted from salivary gland of Haementeria officinalis for treating thrombotic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                When cloned into the yeast expression vector pKH4a2, the sequence forms a fusion product of MAF-alpha-1 leader sequence plus LAPP, which when produced are proteolytically processed by the Lys-Arg cleaving endopeptidase (KEX2), which cleaves on the C terminal side of Lys-Arg, and the products secreted into the culture medium. The LAPP gene was isolated from a leech lambda GT22 cDNA library prepared from total leech salivary gland RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 441 BP; 134 A; 99 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 16; 20pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAQ23871-7.
                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 29776.
                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       ABL26101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL26101 standard; DNA; 1107
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                           27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 TACATTCTGCAAATCAACACAGAAACCAACGAATGCTATAGAAAT 360
                                                            WPI; 2001-656860/75.
                                                                                      Venter JC, Adams M,
                                                                                                                   (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 TTCACCAGCGTCGATGAATGCAGAAAGATGTGCGAAGAATCTGCCGTGGAACCATCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 GATTGCTGGTCTAAACGGCCTGGCTGGAAGCTGCCTGACAATCTGTTGACGAAGACTGAA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 SerSerAspLeuAspGluCysLysLysThrCysPheLysThrGluTyr------Cys 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AspCysTrpThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLysLys 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrIleValPheGluAspThrValAsnLysGluCysTyrTyrAsn 56
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.382
80.50
50.91%
32.73%
14.05%
                                                                                           Li PWD,
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                                                                                          Myers EW;
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01-SEP-2001; 2001WO-EP10074.
                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                       W0200218632-A2
                                                                                                                                                                                                                   Oligonucleotide for detecting cytosine methylation SEQ ID NO 34059.
                                                                                                          HOMO sapiens
                                                                                                                                                                                                                                                              12-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                      ABQ47468 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                  544 GACGGGGATGAGGAGGATGCTGACGAGGATGGGGGATGCTGATGCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1107 BP; 284 A; 313 C; 308 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 -----CTGGACAAGTTGCGGGCAGTGGCCACATCCAGCGACAGCGATGAGAACTACAAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 29776; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 TCCGCCGTGATGCTAAAGGACTACAAAAAGGCA-----TTGAAATATTGCAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                  87 AlaGlyAsnAlaAlaGlyThrGlyAspGluSerAspGluValAspGluAsp 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 GAGTACACAGATGCCGACGAGAGCGTATCCGCGCCCACTGAGTTTCTAGCCGAGTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 ValPheGlu------AspThrValAsnLysGluCysTyrTyrAsnValValAspGly 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 LysSerSerAspLeuAspCluCysLysThrCysPheLysThrCluTyrCysTyrIle 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 LysTyrThrAspPheAspLysSer-----PheLys 23
                                                                                                                                      cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGluLeuAspGlnGluLysPheValVal-------AspGluAsnPheThr 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCTGCAATACGAGCCCGACAACGCCACGGCCAAAGAGTTCTATCCCCTCATC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity:
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77.00
41.88%
23.93%
13.44%
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CD DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one can and the degree of hybridisation to both classes is determined from the two classes of oligomers, the degree of methylation is calculated. The method CC lasses of oligomers, the degree of methylation is calculated. The method CC is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation. The method allows the compliant (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the control of the cantral represent genomic DNA sequences used to illustrate the central for determining the degree of cytosine methylation described in the disclosure of the invention
12-JUL-2002 (first entry)
                                                                                     ABQ47469 standard;
                                                                                                                                                               422 AGCGATTCGACGGGGGGTTTGGACGATTATTACGATGAGGAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 587 BP; 97 A; 81 C; 214 G; 195 T; 0
                                                                                                                                                                                                                                              362 GTTAAGGAGAATATGGTTCGTTTTGTGTTTCGGCGTCGAGTTGGGTAACGGTTTCGGTAGT 421
                                                                                                                                                                                                                                                                                                                                 317 AACGATTGCGTGTGCGACGGT-----TTCGAGCGGTTTATTTGC---GAGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                  257 ACGGACGAATGTCGTATCGTTATTGAGGATATGTTGGTTATGTTTAAGGCCGCGTTGTTT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining the degree of cytosine methylation in genomic DNA, use for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
                                                                                                                                                                                                        94 GlyAspGluSer------AspGluValAspGluAsp 103
                                                                                                                                                                                                                                                                                    74 PheThrGluAsnTyrLeuThrAspCysGluGlyLysAspAlaGlyAsnAlaAlaGlyThr 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 ThrGluTyrCysTyrTleValPheGluAsp-----ThrValAsnLysGluCysTyrTyr 55
                                                                                                                                                                                                                                                                                                                                                                       Asn-----ValValAspGlyGluGluLeuAspGlnGluLysPheValValAspGluAsn 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.78
76.50
48.65%
35.14%
13.35%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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Query Match:
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                                                                                                                                                                   δÃ
                                                                                                                                                                                                       US-09-936-737A-2 (1-103) x ABQ47469 (1-587)
                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC provided to the convert CC provided to the part of the genomic CC The amplicon is hybridised to to uracil, then part of the genomic CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

CC method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 587 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amplicons from chemically treated DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-2001; 2001WO-EP10074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for detecting cytosine methylation SEQ ID NO 34060.
                                                                                                                          331 ACGGACGAATGTCGTATCGTTATTGAGGATATGTTGGTTATGTTTAAGGCGGCGTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200218632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
74 PheThrGluAsnTyrLeuThrAspCysGluGlyLysAspAlaGlyAsnAlaAlaGlyThr 93
                                                                                                                                                  38 ThrGluTyrCysTyrIleValPheGluAsp-----ThrValAsnLysGluCysTyrTyr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                 disclosure of the invention.
                                                                                Asn-----ValValAspGlyGluGluLeuAspGlnGluLysPheValValAspGluAsn 73
                                                     AACGATTGCGTGTGCGACGGT-----TTCGAGCGGTTTATTTGC---GAGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-1043826
2000DE-1044543
                                                                                                                                                                                                                                                                                                                                                                                          195 A; 214 C;
                                                                                                                                                                                                                                            1.78
76.50
48.65%
35.14%
13.35%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin
                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K, Guetig D;
                                                                                                                                                                                                                                                         Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                            <u>ი</u>
                                                                                                                                                                                                                                                                                                                     Matches:
                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                                                          Τ,
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                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                          587
26
10
25
13
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US-09-936-737A-2 (1-103) x AAX20297
                                        Query Match:
                                                    Percent Similarity:
Best Local Similarity:
                                                                                            Pred. No.:
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                  AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes, spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
                                                                                                                                  Sequence 2496
                                                                                                                                                                                                                                                                                          Claim 1; Page 1026-1028; 1128pp; English.
                                                                                                                                                                                                                                                                                                                New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, preventionand therapy of infections, particularly Lyme disease
                                                                                                                                                            Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-081217/07
                                                                                                                                                                                                                                                                                                                                                                                                     White
                                                                                                                                                                                                                                                                                                                                                                                                              Clayton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09858943-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX20297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX20297 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AGCGATTCGACGGGGGTTTGGACGATTATTACGATGAGGAT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 GTTAAGGAGAATATGGTTCGTTTGTGTTTCGGCGTCGAGTTGGGTAACGGTTTCGGTAGT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 GlyAspGluSer---
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                             Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0050359.
97US-0053344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0057483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US12764.
                                                                                                                                871 A;
                          13.3
76.00
48.61%
25.00%
13.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2496
                                                                                                                                  348
                                                                                                                                                                                                                                                                                                                                                                                                              Fraser
                                                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -AspGluValAspGluAsp 103
 (1-2496)
                                                                                                                                  235 G;
                                     Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                            Lathigra
                                                                                                                                  1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sing fever; Lyme detection; ds.
                                                                                                                                  <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                             ,7º
                                                                                                                                  13 other;
                        2496
18
17
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12
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                                                                                                                                                                                                                                                                                                                               prevention
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RESULT 8
AAO7990 IID AAO779
XX AAO779
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XX Huma
DE Huma
XX Huma
XX Huma
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                                                                                        Query Match:
                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                             Alignment Scores:
US-09-936-737A-2 (1-103) x AAQ79969 (1-1399)
                                                                                                                                                                                                                                                                                                                                                                                        AAQ79969 encodes AAR66769 human interleukin-1 beta converting enzyme homolog (Ice-4), increasing Ice-4s enzymatic activity can promote the programmed cell death of cancer cells (pref. those overexpressing the bcl-2 oncogene), this can be used as the basis of a new cancer treatment. Alternatively by reducing Ice-4s enzymatic activity programmed cell death can be inhibited, this may be useful in the development of new cell lines which remain viable in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promoting or preventing programmed cell death in vertebrate cells - by inhibiting the activity of interleukin-1 beta converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9500160-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oncogene bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human interleukin-1 beta converitng enzyme homolog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human interleukin-1 beta convering enzyme homolog (Ice-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ79969 standard; cDNA; 1399 BP
                                                                                                                                                                                                                                                                                                      Sequence 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Fig 16; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR66769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1994;
                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 AAAGAAAAAGAKATAATTCAAAAAACTCTTAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AGAAAAGAAAGATACCTAAARACAAGYAATRTAATAKCAGTTGAAAAAAGARCAAATATCY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 GAA-----TATAAAGAGCAAGAATGGTTTATTTATTTAGCTATCTTATA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GlnGluLysPheValValAspGluAsnPheThrGlu 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 AsnLysGluCysTyrTyrAsnVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 GluCysLysThrCysPheLysThrGluTyrCysTyrIleValPheGluAspThrVal 49
                                                                                                                                                                                                                                                                                                                                                              extended or indefinite periods, independant of growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1995-051742/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0080850
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3..1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           programmed cell death; cancer treatment; ss
                                                                                                                                                                                                                                                                                                         440 A; 270 C;
                                                        7.29
75.50
54.79%
35.62%
13.18%
                                                                                                                                                                                                                                                                                                            316 G;
                                                                                        Conservative: Mismatches: Indels:
                                                                                                                                                                                    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ValAspGlyGluGluLeuAsp
                                                                                                                                                                                                                                                                                                            373 T;
                                                                                                                                                                                                                                                                                                            0 other;
                                                                  26
14
14
19
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RESULT 9
AAT31554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ωy
                                                                              Score:
                                                   Alignment Scores
 Best Local Similarity:
            Percent Similarity:
                                                                                                                  A novel murine cell death gene (AAT31554), designated Ich-3, was identified as a member of the ICE/ced-3 family. It codes for a protein (AAR98464) that shows homology to mouse interleukin-1 beta converting enzyme (ICE), mICh-2 (see also AAR98461) and human Ich-1 (see also AAR98462-63). Full-length ICh-3 cDNA was isolated from a mouse thymus cDNA library. Expression of Ich-3 can be used in methods of regulating cell death, while antisense sequences may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT31554 standard;
                                                                                                                                                                                                                              Claim 21; Fig 14; 127pp; English.
                                                                                                                                                                                                                                                                 Preventing or promoting programmed cell death in vertebrate cells comprises inhibiting or increasing the activity of interleukin-1-beta converting enzyme, or altering expression of
                                                                                                                                                                                                                                                                                                                                                              Miura M,
                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9620721-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ich-3; murine ICE-ced-3 homologue; programmed cell death;
apoptosis; interleukin-1 beta converting enzyme; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ich-3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT31554;
                                                                            Sequence 1399 BP;
                                                                                                        used to prevent programmed cell death.
                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR98464.
                                                                                                                                                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL
                                       No : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 GAACAGCTGAGTTTACAATTTTCTAATGATGAGGATGAT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 TTCTTAGAGAAAACAGACATGGCAGGAAAAATATTTGCTGGCCACATTGCCAATTCCCAG 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGluGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTTTGATGACCTGGTGGAGAAG-----AATGTTTTAAATGGAGATGAGTTG
                                                                                                                                                                                                                                                                                                                                     1996-333763/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspGlu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrLeu-----ThrAspCysGluGlyLys---AspAlaGlyAsnAlaAlaGlyThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAAAATAGGGGAAAGTGCGAGTTTCATCCTGAACAAGGCTGAGAATCTGGTTGAGAAC
                                                                                                                                                                                                                                                        related genes
                                                                                                                                                                                                                                                                                                                                                              Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0368704
                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US00177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --AspGlnGluLysPheValValAsp-----GluAsnPheThrGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
3..1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                               440 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA; 1399
7.29
75.50
54.79%
35.62%
                                                                                                                                                                                                                                                                                                                                                                                          CORP
                                                                                 270
                                                                                 Ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAspGluValAsp 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВÞ
                                                                                 316 G;
  Mismatches:
               Matches:
Conservative:
                                                                                 373
                                                                                 Τ,
                                                                                 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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PF XX PR XX PR XX PR XX PR XX
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DB:
                    Yuan J,
                                                                                                                            16-APR-1998;
                                                                  (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                   14-APR-1999;
                                                                                                                                                                                                                                          21-OCT-1999
                                                                                                                                                                                                                                                                                              W09952925-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine caspase-12 splice variant, caspase-12L cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ32645 standard; cDNA; 1402 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 GAACAGCTGAGTTTACAATTTTCTAATGATGAGGATGAT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
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                    Morishima N;
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/number= 2
304..1402
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AAZ32649"
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94..303
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                                                                           ced-3; virally induced cell death; apoptosis; gene therapy; neural;
muscular degenerative disease; myocardial infarcation; stroke; aging;
interleukin-lbeta converting enzyme; ICE; mouse;
                                                             Ice-ced 3 homologue; Ich; ss
                                                                                                                                                                                                  Mouse Ice-4 coding sequence
                                                                                                                                                                                                                                                       09-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                     AAA72843;
                                                                                                                                                                                                                                                                                                                                                                  AAA72843 standard; DNA; 1402 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1402 BP; 442 A; 270 C; 315 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 GAACAGCTGAGTTTACAATTTTCTAATGATGAGGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 TTCTTAGAGAAAACAGACATGGCAGGAAAAATATTTGCTGGCCACATTGCCAATTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 CTCAAAATAGGGGAAAGTGCGAGTTTCATCCTGAACAAGGCTGAGAATCTGGTTGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 ValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGluGluLeu 63
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                                                                                RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the mouse Ice-4 protein coding sequence. The protein sequence of the present sequence was used in a sequence homology comparison with the protein sequences of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine interleukin-1beta converting enzyme (mICE) (AAB14254), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14260). The present sequence is a member of a family of genes involved in programmed cell death (apoptosis). Ich-1 may play an important role in both the positive and negative regulation of apoptosis. The Ich gene may be used in gene therapy in disorders characterised by cell death e.g. neural and muscular degenerative diseases, myocardial infarcation, stroke, virally induced cell death and aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human Ich-1L and Ich-1S proteins for negative and positive regulation of programmed cell death and for developing therapeutic methods for diseases and conditions characterized by cell death, e.g. myocardial infarction or stroke .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-464343/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yuan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1402 BP; 442 A; 270 C; 315 G; 375 T; 0 other;
            ABL10668;
                                               ABL10668 standard;
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                                                                                                                                                                                                                                              168 CTCAAAATAGGGGAAAGTGCGAGTTTCATCCTGAACAAGGCTGAGAATCTGGTTGAGAAC 227
                                                                                                                                                                               228 TTCTTAGAGAAAACAGACATGGCAGGAAAAATATTTGCTGGCCACATTGCCAATTCCCAG
                                                                                                              288 GAACAGCTGAGTTTACAATTTTCTAATGATGAGGATGAT 326
                                                                                                                                                                                                                                                                                                                                             44 ValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGluGluLeu 63
                                                                                                                                                                                                                                                                              64 -----AspGlnGluLysPheValValAsp-----GluAsnPheThrGluAsn 77
                                                                                                                                               95 AspGlu-----SerAspGluValAsp 101
                                                                                                                                                                                                                                                                                                               GTTTTTGATGACCTGGTGGAGAAG------AATGTTTTAAATGGAGATGAGTTA 167
                                                                                                                                                                                                             TyrLeu-----ThrAspCysGluGlyLys---AspAlaGlyAsnAlaAlaGlyThrGly 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miura M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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US-09-936-737A-2 (1-103) x ABL10668 (1-4453)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0.1840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 26486; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4453 BP; 1232 A; 1020 C; 1060 G; 1141 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                               2175 GCTCGCTGGAATCTTCCGGTTTACTTCCAAATATGCTTT-----CAAGTATGTAAATAA 2228
                                                                                                                                                                                                                                                                                                                                                                                      2124 GAGCAGGCCGTAACGTTCTATCGCCAGCACAAGCAAACA-----AAAAGTTTTGAG 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABB57737-ABB72072)
                                                                  2286 TTTGAAGCCCAGTTGGAGCCGGTGCTCCAGGAGGATAGTTTAAAAGATAAT---CTCACC 2342
                                                                                                                                                                         2229 GTTTATATAGTA----GAATTTTCGATTAATGTGAAATGCTTCTAGGAAATTGCTGGTAAA 2285
                                                                                                                                                                                                                           42 ---TyrIleValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGly 60
                                                                                                                                                                                                                                                                                                                            24 LysSerSerAspLeuAspGluCysLysThrCysPheLysThrGluTyrCys----- 41
             81 AspCysGluGlyLys---AspAlaGlyAsnAlaAla 91
                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GluAspCysTrpThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-656860/75.
                                                                                                                    GluGluLeuAspGlnGluLysPheValValAspGluAsnPheThrGluAsnTyrLeuThr 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-191637P.
2000US-0614150.
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32.61%
13.18%
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Gaps:
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                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                  The invention relates to primers for synthesising full length cDNA clones, 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5' - and 3' -ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                            Sequence 2149 BP; 659 A; 415 C; 531 G; 544 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID NO 4066; 1380pp + sequence listing; English.
                              710 TCCCTATCATTTTGATAATTCCTGGAAAGCATTTCTAGGAGAATTAACTCTTCAGCTTCT 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          830 Primers useful for synthesizing full length cDNA clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human full-length cDNA, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2343 GATAGTGACTACAAAATATCCGCATTTAATGCCGCG 2378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK94875 standard; cDNA; 2149 BP
27 AspLeuAspGluCysLysLysThrCysPheLysThrGluTyrCysTyrIle-ValPheGl 46
                                                                  AspLysSerPhe----
                                                                                      AAAAGAAGAGACTGTTGGTATTTTTTCCCCCTTTGTCTGTAAAGTTAAATATTGTGATTTC
                                                                                                                GluargGluaspCysTrpThrPheTyr-----AlaAsnArgLysTyrThrAspPhe 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-524255/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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75.00
41.51%
25.47%
13.09%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO: 4066
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                                                                                                                                                                             2149
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                                                            ----LysLysSerSer 26
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ABV25467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                 (e) selecting a composition for inhibiting prostate cancer in a patient;(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient;(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                Claim 1; Page 5054; 11750pp; English.
                                                                                                                                                       cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                Schlegel R, Endege WO,
                                                                                                                        in a patient
                                                                                                                               (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             827 AGAGTCAAGCAATCAGTTCCTGATTTATGTTCATTCAAAAGGTGAAGATGTAGAGAAACA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              770 TCCTGCACAGAGTTTAATTGAAAATTTTTCCGAAAGGAGTAT---TACATTGATGAGTTC 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 uAsnTyrLeuThrAsp 81
                  is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                monitoring the progression of prostate cancer in a patient; assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGluGluLeuAspGlnGl 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAATGTTAGAAGAT 962
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-211314P.
2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PheValValAspGluAsnPheThrGl 76
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Sequence 2562 BP; 970 A; 365 C; 641 G; 576 T; 10 other;

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Score:
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                              04-FEB-2000;
24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
10-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAR-2000;
07-JUN-2000;
28-JUN-2000;
28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39265.
                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK84453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      657 GAAAAAAAACATTGTTCAACATACTACAGACTCTTCTCTCGAAGAAAAACAAAGGACATT 716
                                                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                   WO200157182-A2
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 26-JUL-2000;
26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           831 AAACTCAACAGATGGTGAAATGTGTGACAAAGATGCTCTGGAGGAAGATTCAGAAAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          717 AGACTCAGGCACCTCTGAAATTGTGAAATCTCCCAGAATCGAGTGTTCTAAGACA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 eLysThrGluTyrCysTyrIleVal---PheGluAspThrValAsnLysGluCysTyrTy 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 eAspLysSerPheLysLys-----SerSerAspLeuAspGluCysLysLysThrCysPh 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 pAlaGlyAsnAlaAlaGlyThrGlyAspGluSerAspGluValAspGluAsp 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GluArgGluAspCysTrpThrPheTyr-----AlaAsnArgLysTyrThrAsp-Ph 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -AGAAGAGAAATGCAATCAGTGGTTCAACTCATAATGACAAGAGACAGTGATGGTTATGA 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAGGTGATGACGATGGAAGTGAAGATGAAGAGGAG---GATGAAGAT 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GluAsnPheThrGluAsnTyrLeuThrAspCysGluGlyLysAs 86
 ; 2000US-0205515.

2000US-0214886.

2000US-0215135.

2000US-0216847.

2000US-0216880.

2000US-0217487.

2000US-0217496.

2000US-0217496.

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2000US-0219644.
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2000US-0189874.
2000US-0190076.
2000US-0198123.
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2000US-0184664
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(HUMA-) HUMAN GENOME SCI INC

Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 39265; 3071pp + Sequence Listing; English.

CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc arctivity, and can be used in gene therapy and vaccine production. (I) cc proteins and polynucleotides may be used in the prevention, diagnosis and cc example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome cs supplement the patients own production of (I). Additionally, (I) cc polynucleotides may be used to produce the secreted (I), by inserting cc diagnose and treat immune/haematopoietic-related diseases, especially cc cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cc AAK87694 represent human immune/haematopoietic antigen genomic

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                                                                                                                                                                                                                                                                                                                                                                                                     represent sequences used in the exemplification of the present invention
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644 GAGCTG 649
                                                     596 TACTTAGTTTTCCATGATGCC----
                                                                                                       536 TCTGAGCTGTTTACAACTGACCACTGTGTTCCACAGATGTATTTTTCAATAGCTTTTTGT 595
                                                                                                                                                                 42 TyrileValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGlu 61
                            62 GluLeu 63
                                                                                                                                  26 SerAspLeu------AspGluCys---LysLysThrCysPheLysThrGluTyrCys 41
                                                                                                                                                                                            7 TrpThrPhe---TyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLysLysSer 25
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Job time : 233 secs Search completed: February 25, 2003, 02:38:20

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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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| 45                | 44          | 43           | 42           | 41           | 40        | 39           | 38        | 37               | 36                | 3<br>5         | 34            | ω<br>ω      | 32          | 31          | 30         | 29    | 28        | 27         | 26           | 25            | 24         | 23              | 22             | 21           | 20            | 19            | 18              | 17            | 16            | 15             | 14                | 13                |
| 61.5              | ۳.          | μ.           | _            | ۲.           | 1         | ۳            |           | ۲                | ٠,                | 1.             | -             | 62          | 62          | 62          | 62.5       | 63    | 63        | ω          | 63.5         | w<br>·        | 64         | 5               | 65.5           | 5            | 5             | 5             | 6               | 6             | 67            | 67             |                   | 7.                |
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| 2191              | w           | ω            | 1353         | 1345         | 1251      | 1251         | 1251      | 988              | 988               | 954            | 954           | 38          | 28804       | 38          | 10091      | 5285  | 5285      | 11309      | 2735         | 2735          | 2276       | 4524            | 4107           | 2560         | 1647          | 1179          | 7295            | 261           | 3110          | 2143           | 4379              | 4379              |
| 4                 | 4           | w            | N            | N            | 4         | w            | N         | 4                | 4                 | 4              | 4             | w           | ω           | N           | ω          | 4     | N         | 4          | u            | N             | 4          | 4               | N              | 4            | 4             | 4             | 2               | 4             | 4             | 4              | ω                 | н                 |
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| Sequence 1, Appli | 9 0         | D (          | D :          | ω            | uence 2,  | 1ce 2,       | e<br>2    | e 34,            | Sequence 34, Appl | e 37,          | 37, App       | 2, Appl     | Ν.          | e 1, Appl   | e 34, App  | e 29, | e 29, App | e 108, Ap  | e 1,         | equence 1     | equence 56 | equence 7, Appl | e 24           | equence 11   | equence 5,    | equence 25    | e<br>15         | e 11          | e 25          | 21             | Sequence 17, Appl | 17                |

## ALIGNMENTS

US-08-741-134-1

Sequence 1, Application US/08741134 Patent No. 5851498

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark GENERAL INFORMATION: APPLICANT:
APPLICANT: COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: Wodderfect for Windows 6.1
CURRENT APPLICATION DATA: COMPUTER READABLE FORM: TITLE OF INVENTION: NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: TITLE OF INVENTION: CLASSIFICATION: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz STREET: One Liberty Place - 46th floor CITY: Philadelphia NAME: DeLuca, Mark REGISTRATION NUMBER: APPLICATION NUMBER: REFERENCE/DOCKET NUMBER: COUNTRY: Pennsylvania Litwack, Gerald Alnemri, Emad S. Fernandes-Alnemri, Teresa METHODS OF USING THE SAME AND IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING US 60/007,163 US/08/741,134 TJU-2090 No. 5861498ris

Patent

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TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100

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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08044547 Patent No. 5324715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         APPLICANT: Connolly, Thomas M.
APPLICANT: Keller, Paul M.
TITLE OF INVENTION: Protein for Inhibiting
TITLE OF INVENTION: Collagen-Stimulated Platelet Aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 GAGGAAACTCGAGAATGCCAATGATGCCACAGCTAACAAAAAGGCCCAAGCCTGACAAGAA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                705 AATGAAC-----ACATCAGCTGAAGGAGATGACAGTGATGAAGAGGATGATGATGAAGA 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 sPheLysThrGluTyrCysTyrIleValPheGluAspThrValAsnLysGluCysTyrTy 55
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                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  APPLICATION NUMBER:
                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                             CITY:
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US/08/044,547
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Best Local Similarity:
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Patent No. 5324715
GENERAL INFORMATION:
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APPLICATION NUMBER: US 07/594,917
FILING DATE: 09-0CT-1990
ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/594,917
FILING DATE: 09-OCT-1990
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Protein for Inhibiting TITLE OF INVENTION: Collagen-Stimulated Platelet Aggregation
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Connolly, Thomas APPLICANT: Keller, Paul M.
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                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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FILING DATE:
                                                                         FILING DATE:
                                                                                              APPLICATION NUMBER: US/08/044,547
                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                ADDRESSEE: Merck & Co., Inc. STREET: P.O. Box 2000
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ATTORNEY/AGENT INFORMATION:

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US-08-258-287B-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Buggisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920001
                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
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                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 TACATTCTGCAAATCAACACAGAAACCAACGAATGCTATAGAAAT 360
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
TELEPAX: (908) 594-4720
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                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 TELEPHONE:
                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 10-JU
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Best Local Similarity:
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TELEX: 248636 SKR
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1402 base pairs
APPLICATION NUMBER: US 08/080,850 FILING DATE: 24-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10-JUN-:
                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 GAACAGCTGAGTTTACAATTTTCTAATGATGAGGATGAT 326
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                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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STRANDEDNESS: both
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Best Local Similarity:
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REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
TELEFAX: (208) SSK
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 199, Application US/08961083 Patent No. 6159469
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LENGTH: 1402 base pairs
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                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
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                                                       CLASSIFICATION: 435 PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
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LOCATION: 45.
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                      FILING DATE:
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                                         APPLICATION NUMBER:
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1: 9410 Key West Avenue
Rockville
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                ; sequence 71, Application US/08961527; Patent No. 6420135; GENERAL INFORMATION: APPLICANT: Charles Kunsch
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1226 GCTTATTTTGGTCAAGAA 1243
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                                                     CURRENT APPLICATION DATA: US APPLICATION NUMBER: US
PRIOR APPLICATION DATA:
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STRANDEDNESS: doub
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                                                                                                     COMPUTER: HP Vect
OPERATING SYSTEM:
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                                                                                                                                                                                                                         STATE:
                                      FILING DATE:
                                                                                                                                                                                                   COUNTRY:
                   CLASSIFICATION:
                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                    ZIP:
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                                                                                          SOFTWARE: ASCII Text
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                                                           us/08/961,527
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                                                                                                                                                 3.50 inch, 1.4Mb storage
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: FILING DATE:

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CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
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Best Local Similarity:
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US-08-961-527-71
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                                                                                                                                                                                                                                                                                                                                           Sequence 151, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
EARLIER APPLICATION NUMBER: 60/040,626 EARLIER FILING DATE: 1997-03-07 EARLIER APPLICATION NUMBER: 60/040,334 EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7462 GCTTATTTTGGTCAAGAA 7479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7402 TIGITIGCTACAGACITACAAGATTATCCTTTGGCTGCTGTTAGAGATTTTGGGGGCAGA 7461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7342 CAAGAAGACAAGGCCCTCTACTTGGACTGTGATCTAGTTGTAACGAAAAATCTGGATGAC 7401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7243 GAAATTATTAATTGTCGGGTAACTTCTGAGCAAATTTCATGTTATAAATCGGATATTAGT 7302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7201 TGGATTAAGCAATTAAATAAGCGCTTAGAGAAGTTTGAC-----TCA-7242
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LENGTH: 32768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7303 TACACAGTCTTT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AlaGlyThrGlyAspGlu 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 AsnTyrLeuThrAspCysGluGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GluLeuAspGlnGluLysPhe------ValValAspGluAsnPheThrGlu 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 TyrileValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGlu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 AspLeuAspGluCysLysLysThr------CysPheLysThrGluTyrCys 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TrpThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLysLysSerSer 26
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(301) 309-8512
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Matches:
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| 1997-04-11<br>NUMBER: 60/043<br>1997-04-21<br>NUMBER: 60/043<br>1997-04-11<br>NUMBER: 60/043<br>1997-04-11<br>NUMBER: 60/043<br>1997-04-11<br>NUMBER: 60/043<br>1997-04-11<br>NUMBER: 60/043<br>1997-04-11 | 1997-05-23<br>NUMBER: 60/04<br>1997-05-23<br>NUMBER: 60/04<br>1997-05-23<br>NUMBER: 60/04<br>1997-05-23<br>NUMBER: 60/04<br>1997-04-11<br>NUMBER: 60/04<br>1997-04-11<br>NUMBER: 60/04<br>1997-04-11<br>NUMBER: 60/04<br>1997-04-11<br>NUMBER: 60/04<br>1997-04-11<br>NUMBER: 60/04<br>1997-04-11<br>NUMBER: 60/04<br>1997-04-11<br>NUMBER: 60/04               | INUMBER: 60/04   | N NUMBER: 60/04<br>E: 1997-03-07<br>N NUMBER: 60/04 |
| 7 1 7  | ,61<br>,63<br>,58<br>,58<br>,56<br>,56<br>,56<br>,56  | 7,60<br>7,50<br>7,59<br>7,59<br>7,61<br>7,61<br>7,58<br>7,58<br>7,58<br>7,58<br>7,58<br>7,58<br>7,58<br>7,58   | 0,336<br>0,163                                      |

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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,893
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APPLICATION NUMBER: 60/047,595
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,892
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APPLICATION NUMBER: 60/057,761
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APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11
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                                                                                                              877 CTAGCAGCAATGACGCCTGCAAACAGCAGAGCTGACAGAGATTATGGGCACAGATTCAGGA 818
                                                                                                                                                                                   934 ATTACATTTTCTTGC---AGCAACTGTGTCACAGTTAAATCAAAGGACCAAAGACCGATT 878
                                                                                                                                                                                                                                                     994 AGATCAAGAAGATAGTTCATGGAGTTCTGTACACCATTTATAATGCCTCTTTCAGATTCA 935
                                                  817 CTTGTCTCCGGGACA
                                                                                                                                                                                                                49 ValAsnLysGluCysTyrTyrAsnValValAspGlyGluGluLeuAspGlnGluLysPhe 68
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                                                                                  89 AsnAlaAlaGlyThr 93
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APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/056,664
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Indels:
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; Sequence 21, Application US/08484105
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GENERAL INFORMATION:

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Best Local Similarity:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-4187
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STREET: 4
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-----GluLysPheValValAspGluAsnPheThrGluAsnTyrLeuThrAspCysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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HERSKOWITZ, Ira
LI, Joachim J
GAVIN, Kimberly
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McNALLY, Francis J
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KOBAYASHI, Ryuji
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Matches:
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Indels:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1676 base pair
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
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(415) 494-8771
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FOSS, Margit
MCNALLY, Francis J
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HERSKOWITZ, Ira
LI, Joachim J
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              8.26
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              Conservative: Mismatches: Indels:
Gaps:
                                                              Matches:
                                                                               Length:
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US-09-936-737A-2 (1-103) x US-08-484-106-21 (1-1676)

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EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER APPLICATION NUMBER: 60/047,593
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US-09-149-476-289/c
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Patent No. 642052
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CURRENT APPLICATION NUMBER: US/09/149,476
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                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/400,179
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 389,922
FILING DATE: 18-JUN-1982
FILING DATE: 18-JUN-1982
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 60/049,610 EARLIER FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
11 AlaAsnArgLysTyrThrAspPheAspLysSerPheLysLysSerSerAspLeuAspGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             767 ACGAGCAAGCCAAAAGCTTCAGGATTTGGA---GCCAGGATGACCATGATGAAATGCAGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               827 TTTTGGGCAAATCGGAAATACATAATGTGGCCCATTGCCACAAAGGAGACTGAAATCAAT 768
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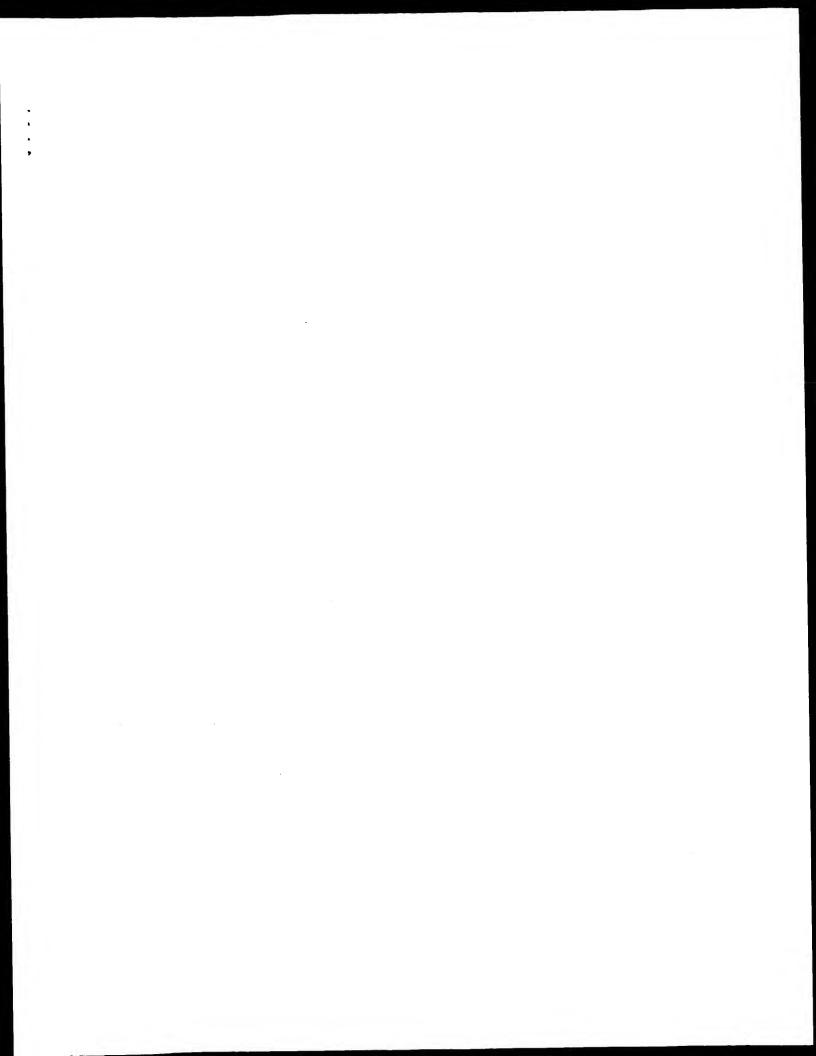
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GENERAL INFORMATION:
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                                            Best Local Similarity:
Query Match:
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US-09-936-737A-2 (1-103) x US-08-592-214A-17 (1-4379)
                                                                               percent Similarity:
                                                                                               Score
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
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TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
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CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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OTHER INFORMATION: /not
OTHER INFORMATION: thal
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OTHER INFORMATION: nucleotides."
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LOCATION:
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thaliana AP1 gene"
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                                                                                  Alignment Scores:
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   Query Match:
                    Percent Similarity:
Best Local Similarity:
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APPLICANT: Yanofs
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INFORMATION FOR SEQ ID NO:
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ADDRESSEE: Campbell & Flores LLP
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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OTHER INFORMATION: /I
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thaliana AP1 gene"
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Best Local Similarity:
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; ORGANISM: Drosophila melanogaster
US-09-069-023-21
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US-09-069-023-21
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APPLICANT: NOBER, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-0333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
LENGTH: 2143
TYDE: NNA
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GENERAL INFORMATION:
                                                                       554 GGAGAGCTGAACGGAGGAGGGCGACACCACCGAT 592
                                                                                                                                                                                                                                  437 CGCACCCTCGACGAGAAT---ACGGAACTGGTGGCCGTCTTTCCCGGAGAACATTGGATC 493
                                                                                                                                                    494 GATCCCACTCACTACGTGACGATAACCACTCCACATGGCAACGAGGCAGGAACTGGAAAC 553
                                                                                                                                                                                                                                                                                                                     392 CACCTGGACTCC-------GACGGCACGGAGATCGATGATGAGGAGTACTTT 436
                                                                                                                                                                                                                                                                                                                                                                                                   338 ATCCGCAGCAAGGTGGCGGAGAAGTTCGAGAAGTGCGACCACCTG-----CCCACCATC 391
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                                                                                                  89 ------AsnAlaAlaGlyThrGlyAspGluSerAsp 98
                                                                                                                                                                                         77 ------AsnTyr------ LeuThrAspCysGluGlyLysAspAlaGly----- 88
                                                                                                                                                                                                                                                                              69 ---ValValAspGluAsnPheThrGlu------
                                                                                                                                                                                                                                                                                                                                           50 AsnLysGluCysTyrTyrAsnValValAspGlyGluGluLeuAspGlnGluLysPhe--- 68 ::: :::
                                                                                                                                                                                                                                                                                                                                                                                                                                        31 CysLys---LysThrCysPheLysThrGluTyrCysTyrIleValPheGluAspThrVal 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LysTyrThrAspPheAspLysSerPheLysLys-----SerSerAspLeuAspGlu 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ThrAspPheAspLysSerPheLysLysSerSerAsp-----LeuAspGluCysLysLys 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 TyrTyrAsnValValAspGlyGluGluLeuAspGln 65
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11.69%
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-MODEL-frame+_p2n.model -DEV-xlh
-Q-/cgn2_1/USPTO_spoo1/US09936737/runat_14022003_100733_2323/app_query.fasta_1.263
-DB-Published_Applications_NA _QFWT-fastap -SUFFIX-rnpb -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START=1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFMT-pto -NOME-ext -HEAPSIZE=500 -MINLEN-0
-MAXLEN-200000000 -USER-US09936737_eCGN_1_1_33_erunat_14022003_100733_2233
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-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS=1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                       C
                                                                                                                                          No.
                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                          Score
     71.5
70.5
70
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Match Length DB ID
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11:
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13:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                                 1092
543
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  10 US-09-815-242-9446
9 US-09-796-692-9477
9 US-10-040-739-838
10 US-09-815-242-7425
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933.046 Million cell updates/sec
Sequence 9446, Ap
Sequence 9477, Ap
Sequence 838, App
Sequence 7425, Ap
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|---|--|
| 6033355544455555555555555555555555555555  | 70<br>69.5<br>68   |
|   | 12.2<br>12.1<br>11.9   |
| 515<br>515<br>2664<br>2664<br>1402<br>33110<br>33110<br>33110<br>33110<br>33110<br>33110<br>33110<br>340681<br>2155<br>562<br>562<br>562<br>562<br>562<br>562<br>562<br>5   | 197997<br>2023<br>1861<br>1988                                   |
| 11100000000000000000000000000000000000  | 10   |
| US-09-78-89-79 US-09-910-943-179 US-09-9130B-51 US-09-759-130B-51 US-09-959-900-257 US-10-149-110-10 US-09-9110-1574-56 US-09-910-988-1 US-09-970-988-1 US-09-970-988-1 US-09-970-988-1 US-09-970-988-1 US-09-974-298-113 US-09-974-298-113 US-09-974-298-113 US-09-974-298-113 US-09-974-298-113 US-09-974-298-113 US-09-974-298-113 US-09-974-298-113 US-09-954-456-2125 US-09-954-456-2125 US-09-954-456-2125 US-09-954-456-2125 US-09-954-456-2125 US-09-954-456-2125 US-09-954-456-213 US-09-954-456-213 US-09-954-456-213 US-09-954-456-217 US-09-954-456-217 US-09-958-842A-2486 US-110-042-417-51 US-09-930-871-17 US-09-930-871-768A-1 US-09-930-871-7   | S-09-822-246-<br>S-09-765-272-<br>S-09-729-674-<br>S-09-864-761- |
| sequence 3, Applia sequence 179, App Sequence 179, Applia sequence 51, Applia sequence 51, Applia sequence 51, Applia sequence 270, Applia sequence 10, Applia sequence 10, Applia sequence 10, Applia sequence 13, Applia sequence 14, Applia sequence 1512, Applia sequence 113, Applia sequence 113, Applia sequence 113, Applia sequence 113, Applia sequence 216, Applia sequence 216, Applia sequence 216, Applia sequence 217, Applia sequence 51, Applia sequence 52, Applia sequence 2486, Applia sequence 11, Applia sequence 17, | equence 3, equence 199 equence 129 equence 474                   |

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## ALIGNMENTS

RESULT 1

US-09-815-242-9446/c

Sequence 9446, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REBERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/23,625
PRIOR FILING DATE: 2000-11-27

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US-09-796-692-9477
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FEATURE:
; NAME/KEY: CDS
; LCCATION: (1)...(1092)
US-09-815-242-9446
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9477, Application US/09796692 Publication No. US20020198362A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9446
                                                                                                                                                                                                                                                                                                                         APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Manfolo, Jane
APPLICANT: Manfolo, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
                                                                                 PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/200,303
                                                PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-12-22
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
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FILING DATE: 2000-U3-U1
RIPLICATION NUMBER: 60/202,084
RAPPLICATION NUMBER: 60/202,084
RAPPLICATION NUMBER: 60/206,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 CysTrpThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLysLysSer 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGGGAAGGATGCGATAGCTGC 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrGluAsnTyrLeuThrAspCys 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrAsnValValAspGlyGluGluLeuAspGlnGluLysPheValValAspGluAsnPhe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAATTCCTTTTTCTGCATCCAAGTCTTTACGGATACGACCAACAAAGGTATCACGTGA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCAATCTGAACTGAGTTCCAAGCAGCACCTTTGAGAAGGTTATCTGAAACAACCCACAT 970
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12.48%
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Indels:
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; LOCATION: (436)
; OTHER INFORMATION: n=A,T,C o
; NAME/KEY: unsure
; LOCATION: (485)
; OTHER INFORMATION: n=A,T,C o
US-09-796-692-9477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
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                                                                                                                                                                                                     Sequence 838, Application US/10040739 Patent No. US20020173635A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 9477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/223,378 PRIOR FILING DATE: 2000-08-07 NUMBER OF SEQ ID NOS: 9597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR APPLICATION STATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
No.:
                                                                                                                                                                                                                                                                                                                              376 AGGCAATACGGCCGTGGGCGATCTGGGGGCCAGGTTCGGGATGAGTATCGGCAGGAC 432
                                                                                                                                                                                                                                                                                                                                                                                                                331 GACCGA-----ATCATTCGCACAGACTGGGACGCAGGCTTTAAG------GAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 TATTACTCACGCGCAGATGCGGAAAACGCCATGCGGTACATAAATGGGACGCGTCTGGAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 TACACAACTGAAGAACAAATCTATGAACTCTTCAGCAAAAGTGGTGACATAAAGAAAATC
                                                                                                                                                                                                                                                                                                                                                                     85 LysAspAlaGlyAsnAlaAlaGlyThrGlyAspGluSerAspGluValAspGluAsp 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 PheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGluGluLeuAsp 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GluGluArgGlu-------AspCysTrpThrPheTyrAlaAsnArgLysTyr 15
               Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
CORRESPONDENCE ADDRESS
                                                                                                                                                                                APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnGluLysPheValValAspGluAsnPheThrGluAsnTyrLeuThrAspCysGluGly 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATGGGTCTGGATAAAATGAAGAAAACAGCA----TGTGGATTCTGTTTTGTGGAA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------LeuAspGluCysLysLysThrCysPheLysThrGluTyrCysTyrIleVal 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThraspPheaspLysSer------PheLysLysSerSerAsp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543
                                                                                                                      Racie, Lisa
                                                                                                                                         LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.746
70.50
38.66%
21.85%
12.30%
                                                                                                                                                               John
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                                    EXPRESSED SEQUENCE TAGS
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Matches:
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Indels:
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US-09-815-242-7425
Sequence 7425, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 838:

US-10-040-739-838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                   438 TAGTGAAATAGGAAGTGATGAGGAATCTGAAAATGAAATTACAAGTGTTGGTAGAGCTTC 497
                                                                                                                                                                                                                                                                                                                                                                                319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO.:
                                                                                                                        498 AGGTGATGACGATGGAAGTGAAGATGAAGAG 531
                                                                                                                                                                                                                                                                                  378 AAACTCAACAGATGGTGAAATGTGTGACAAAGATGCTCTGGAGGAAGATTCAGAAAGCGT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 AGACTCAGGCACCTCTGAAATTGTGAAATCTCCCAGAATCGAGTGTTCTAAGACA---- 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 GAAAAAAAACATTGTTCAACATACTACAGACTCTTCTCTCGAAGAAAAAACAAAGGACATT 26:
                                                                                                                                                55 rAsnValValAspGlyGluGluLeuAspGlnGluLysPheValValAspGluAsnPheTh 75
                                                                                                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 eAspLysSerPheLysLys-----SerSerAspLeuAspGluCysLysLysThrCysPh 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GluArgGluAspCysTrpThrPheTyr-----AlaAsnArgLysTyrThrAsp-Ph 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 540 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,520
EILING DATE: 03-JUN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                          rGluAsnTyrLeuThrAspCysGluGlyLysAsp-----AlaGlyAsnAlaAl 91
                                                                                                                                                                                                                                                                                                                                                                                                         eLysThrGluTyrCysTyrIleVal---PheGluAspThrValAsnLysGluCysTyrTy 55
                                                                                                                                                                                                                                                                                                                                                                   -AGAAGAGAAATGCAATCAGTGGTTCAACTCATAATGACAAGAGACAGTGATGGTTATGA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brown, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.866
70.00
43.75%
27.68%
12.22%
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Sequence 3, Application US/09822246;
Patent No. US20020142383A1
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1).
US-09-815-242-7425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3504
TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                             859 --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               718 GATAAAACTGAGCAATCCTCAAACGATCCCAAAGAAGCCCCAAAAAAACCCCTTTTTGACGCT 777
                                                                                                                                                                                                                                                                                                                                                                                                                    778 -----ATCTTGCTGCAAGATCTAGCGAAC-----GCCGTGTATAACGTCATG 819
                                                                                                                                                                                                                                                                 79 LeuThrAspCysGluGlyLysAspAlaGlyAsnAlaAlaGlyThrGlyAspGlu 96
                                                                                                                                                                                                                                                                                                                                                                      59 AspGlyGluGluLeuAspGlnGluLysPheValValAspGluAsnPheThrGluAsnTyr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GluTyrCysTyrTleValPheGluAspThrValAsnLysGluCysTyrTyrAsnValVal 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AspLysSerPheLysLysSerSerAspLeuAspGluCysLysLysThrCysPheLysThr 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind, Judith W. Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu, H. Howard
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                                                                                                                                                                                                                                      --GCTAAAAAAACGGGCAACATCGCAAGGACCTTGAATGAG 897
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70.00
46.15%
30.77%
12.22%
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Indels:
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Matches:
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Db 182546 ACATTTATGACTTTTGAGAGATTTACAACTTTCACAAAGCAGGGAGAGAAAAGTAGGGAC 182487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 199, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001149
CURRENT APPLICATION NUMBER: US/09/822,246
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(197997)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 197997
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                        TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO: 199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 LeuAspGluCysLysLysThrCysPheLysThrGluTyrCysTyrIleValPheGluAsp 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 ThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLysLysSerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: -CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: -CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
TYPE: nucleic acid
                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Maryland
TOPOLOGY:
                       STRANDEDNESS: double
                                                                                                                                                                                                 REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20850
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12.22%
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Best Local Similarity:
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                              Alignment Scores:
                                                                   ; ORGANISM: Homo sapiens US-09-729-674-129
Score:
                Pred. No.:
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                                                                                                                                       SEQ ID NO 129
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                    CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER CO. 2000-03-30
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                                                                                                                                                         SOFTWARE:
                                                                                                                                                                            NUMBER OF SEQ ID NOS: 283
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLECTIDES ENCODING THEM FILE REFERENCE: 6055-64X
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                                                                                                       TYPE: DNA
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Genetics Institute, Inc.
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Steininger II, Robert J.
Spaulding, Vikki
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Treacy, Maurice
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LaVallie, Edward R.
Collins-Racie, Lisa A.
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Percent Similarity:
Best Local Similarity:
Query Match:
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PRIOR FILING DATE: 2000-02-04
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-x-1
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                                                                                                                                                                                                                                         OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
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                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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                                                                            APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                     APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                           APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                 APPLICATION NUMBER: PCT/US01/00661
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2001-01-30
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US-09-727-384-3
; Sequence 3, Application US/09727384
; Patent No. US20020098511A1
; GENERAL INFORMATION:
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                                                                                                                                                                       APPLICANT:
CURRENT APPLICATION NUMBER: US/09/727,384
CURRENT FILING DATE: 2000-12-01
                                                FILE REFERENCE:
                                                             APPLICANT: Bartel, Paul L.
TITLE OF INVENTION: Prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCATATGCCCTCTTCAATCAATTTACTTGTGCAGAATCAGCAGACACCAAACAGTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rCysTyrIleValPhe----
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INFORMATION:
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                                                                                                       Heichman, Karen
Cimbora, Daniel M.
Bush, Angie
Mauck, Kimberly
                                                                                                                                                                                           Myriad Genetics, Inc
                                              2318-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N: EXPRESSED IN PLACENTA, SIGNAL = 1.0

N: EXPRESSED IN HBL100, SIGNAL = 1.5

N: EXPRESSED IN HEART, SIGNAL = 1.5

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

N: EXPRESSED IN HELA, SIGNAL = 1.8

N: EXPRESSED IN HELA, SIGNAL = 1.8

N: EXPRESSED IN BOLTATA SIGNAL = 2.1

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

N: EXPRESSED IN BATATA SIGNAL = 2.1

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                                                                  Protein-Protein Interactions
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PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999

WBER: US 60/168,377 1999-12-02

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CURRENT APPLICATION NUMBER: US/09/798,889

CURRENT FILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,714

PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

PRIOR PPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,686

PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,687

PRIOR PILING DATE: EARLIER FILING DATE: 1998-03-12

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/077,687

PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/077,696

PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-798-889-29; Sequence 29, Application US/09798889; Publication No. US20030004324A1
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; LOCATION: (141)..(2159)
US-09-727-384-3
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LENGTH: 5153
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                                                                          SEQ ID NO 29
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NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human secreted proteins
FILE REFERENCE: PZ026P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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ORGANISM: Homo sapiens
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                                                 ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rCysTyrIleValPhe------GluAspThrValAsnLysGluCysTy 54
                                                   914
                                                                                                    PatentIn Ver. 2.0
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                                                                                                                                      US-09-936-737A-2 (1-103) x US-09-834-975-897 (1-2664)
                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 897
LENGTH: 2664
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Van Huffel, Christophe
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REPERENCE: MRI-0168
FULE REPERENCE: MRI-0168
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/197,538 PRIOR FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lillie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1046
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (1)...(2664)
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                                                            1700 TTCGCTTATCCTTATTGTAATCATGTTTTTGTGGAGACCATCAGCAAACAATCAGAGATA 1759
                                                                                                                                                                                                                                                                                No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 TGAAAATTTAACCGAAGGAATAAAATTAAGAGCC---TCAAAATCAGTTTCCAATGGAAC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 TGCCTTCATGCCCTTAATAGATGATTCTGATGATGAAATTGAGGAATTCATGGTAACTTC 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 pGluAsnPheThrGluAsnTyrLeuThrAspCysGluGlyLysAspAlaGlyAsnAlaAl 91
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53 Cys-TyrTyrAsnValValAspGlyGluCluLeuAspGlnGluLysPheValVal---As 71
                                                                                            36 PheLysThrGluTyrCysTyrIleValPheGluAspThrValAsnLysGlu------
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RESULT 13
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: n may be a or g or c or t/u US-09-910-943-179
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                                                                                                                                                                           GENERAL
                                                                                                                                                                                          Sequence 61, Application US/09759130B Publication No. US20030022279A1
                                                                                               APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 179
LENGTH: 763
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                            APPLICANT:
                                                                                                                                    APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: McCarthy, Sean A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 179, Application US/09910943 Patent No. US20020081610A1 GENERAL INFORMATION:
                                                            APPLICANT:
                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/16148US1
                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-07-23 NUMBER OF SEQ ID NOS: 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/910,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Xenopus laevis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1)..(763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1760 TGCCTTCATGCCCTTAATAGATGATTCTGATGATGAAATTGAGGAATTCATGGTAACTTC 1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1877 AGCTAAGCCTGCCACTTCTGAGAACTTTGATGAAGAT 1913
                                                                                                                                                                                                                                                                                           285 GAAGGTGGCGAT 296
                                                                                                                                                                                                                                                                                                                                                                   243 GCTGAACAAGAGAAAACAACTGTCTCTGAAAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                        195 GTGGAATTCAGTGATCAT---CAAATCCAGTGCTCTAAT-----GATGAGTCATCT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 AAATCATCTAGTGATATCAGTTATTGCCCCAAAAACATCAATTCAGACAGGGCGTATGTCT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1820 TGAAAATTTAACCGAAGGAATAAAATTAAGAGCC---TCAAAATCAGTTTCCAATGGAAC 1876
                                                                                                                                                                                                                                                                                                                                                                                                63 LeuAspGlnGluLysPheValValAspGluAsnPheThrGluAsnTyrLeuThrAspCys 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 IleValPheGluAspThrValAsnLysGluCysTyrTyrAsnValValAspGlyGluGlu 62
                                                                                                                                                                                                                                                                                                                              83 GluGlyLysAsp 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 LysLysSerSerAspLeuAspGluCysLysLysThrCysPheLysThrGluTyrCysTyr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 pGluAsnPheThrGluAsnTyrLeuThrAspCysGluGlyLysAspAlaGlyAsnAlaAl 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 aGlyThrGlyAspGluSerAspGluValAspGluAsp 103
                                                                                                                                                                           INFORMATION:
            Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
                                                                                        McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
Leiby, Kevin R
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67.00
42.19%
32.81%
11.69%
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Conservative:
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US-09-759-130B-51

; Sequence 51, Application US/09759130B

; Publication No. US20030022279A1
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                     Publication:
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
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            APPLICANT:
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PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: US 09/578,063
PRIOR FILING DATE: US 09/578,063
PRIOR FILING DATE: 2000-05-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/333,159 PRIOR FILING DATE: 1999-06-14
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MPI00-5350MNIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 1402
                                                                                                                                                                                                                                                       662 AAA 660
                                                                                                                                                                                                                                                                                                                                         818 AAAACATGTTTCTAAACA---TTTTTATCCCTGACTATGGCCCAAATAGTAAATAAAACA 762
                                                                                                                                                                                                                                                                                                                                                                                                                                       761 GCTCAAGCTTTAGAGGCCCAAGAGACCTATGTAAATGTGTTG
                                                                                                                                                                                                                                                                                                        85 Lys 85
                                                                                                                                                                                                                                                                                                                                                                                65 GlnGluLysPheValValAspGluAsnPheThrGluAsnTyrLeuThrAspCysGluGly 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 LysThrCysPheLysThrGluTyrCysTyrIleValPheGluAspThrValAsnLys--- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/602,871 FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GluCysTyrTyrAsnValValAspGlyGluGluLeuAsp 64
Fraser, Christo
Sharp, John D
Barnes, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
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67.00
42.62%
34.43%
11.69%
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Matches:
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Indels:
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CURRENT ETLING DATE: US/09/759,130B
CURRENT ETLING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILLING DATE: 2000-01-07
PRIOR FILLING DATE: 2000-04-27
PRIOR PPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILLING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR APPLICATION NUMBER: US 09/506,194
PRIOR FILLING DATE: 1999-06-14
PRIOR FILLING DATE: 2000-07-14
PRIOR FILLING DATE: 2000-07-14
PRIOR FILLING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-759-130B-51
                  US-09-939-980-257
Sequence 257, Application US/09939980
Patent No. US20020082234A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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                                                                                                            RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GOOÓGEAT, Andrew
APPLICANT: HOITZMAN, DOUGLAS A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
FILE REFERENCE: MPIO0-5350MNIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/602,871 PRIOR FILING DATE: 2000-06-23 PRIOR APPLICATION NUMBER: US 09/420,707 PRIOR FILING DATE: 1999-10-19
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2330
                                                                                                                                                                                                                                                                                                                                                                                                                    1488 AAAACATGTTTCTAAACA---TTTTTATCCCTGACTATGGCCCCAAATAGTAAATAAAACA 1544
                                                                                                                                                      1644 AAA 1646
                                                                                                                                                                                                                                           1545 GCTCAAGCTTTAGAGGCCCCAAGAGACCTATGTAAATGTGTTG---------
                                                                                                                                                                                                                                                                                                                                                                     52 ------GluCysTyrTyrAsnValValAspGlyGluGluLeuAsp 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 LysThrCysPheLysThrGluTyrCysTyrIleValPheGluAspThrValAsnLys--- 51
                                                                                                                                                                                                                                                                                     65 GlnGluLysPheValValAspGluAsnPheThrGluAsnTyrLeuThrAspCysGluGly 84
                                                                                                                                                                                               85 Lys 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/342,364
FILING DATE: 1999-06-29
APPLICATION NUMBER: US 09/608,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/393,996 FILING DATE: 1999-09-10
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APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wrighton, Nicolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leiby, Kevin R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers, Paul S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mackay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charles R
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 257:
SEQUENCE CHARACTERISTICS:
                                                                            1297 ATAACAGTAAACGATAAAAACGAAGTTATCGGATACGTTAATACTGGCGGTTTACGCAAT 1356
                                                                                                                                                                 1237 TTCTGGAACGAATGCCAACAAAGTTACTATAACTAAAATTATGGGGTGGAAATAATGAAA 1296
                                                                                                                                                                                                                                                       1183 ACCCACTTTAAGAATAGACAACGATGTGTATTT-----CGATTTAGGCAAAACATCAGG 1236
                                                                                                                   47 AspThrValAsnLysGlu-------CysTyrTyrAsnVal-----
                                                                                                                                                                                                      28 Leu---AspGluCysLysLysThrCysPheLysThrGluTyrCysTyrIleValPheGlu 46
                                                                                                                                                                                                                                                                                              8 ThrPheTyrAlaAsnArgLysTyrThrAspPheAspLysSerPheLysLysSerSerAsp 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38,8 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/936,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
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NVENTION: No. US20020082234A1el Prokaryotic Polynucleotides,
NVENTION: No. Polypeptides and Their Uses
                                    -ValAspGly----
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Rosenberg, Martin
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|------|---|--|
| 1524 | Db 1465 AAAGAAGACGTACCGAATGCATCAAGCCAACAAAGTGAATCAGATTTGAGTGATGAAGAA 1524 |  |
| 103  |   |  |
| 1464 | Db 1417 AAGTTTGTTTTCACTAACGGCGAAATTAAATATAACAGCAATTTTGAA 1464             |  |
| 83   | luAs  |  |
| 1416 | Db 1357 AGTTTAGATGTAGATGATAACAATGTGCCTATCAAATTCAAAGAAGAGTTTGAACCTAGA 1416 |  |

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Copyright (c) 1993 - 2003 Compugen Ltd.
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|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------------------|----------|--------|--------|--------|--------------------|--------------------|
| 68.5               | 68.5               | 69                 | 69     | 69                 | 69                 | 69.5   | 69.5   | 69.5   | 69.5               | 69.5     | 70     | 70     | 70     | 70                 | 70.5               |
| 12.0               | 12.0               | 12.0               | 12.0   | 12.0               | 12.0               | 12.1   | 12.1   | 12.1   | 12.1               | 12.1     | 12.2   | 12.2   | 12.2   | 12.2               | 12.3               |
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| 2                  | Ν                  | N                  | N      | N                  | N                  | N      | N      | N      | N                  | <u>-</u> | N      | 2      | Ν      | N                  | N                  |
| D70100             | T26487             | T18444             | T28317 | T33328             | T32824             | AI3625 | D95206 | S61160 | T37899             | PSPGA    | B97104 | F71909 | S50295 | T24432             | C86406 ·           |
| phosphoglucomutase | hypothetical prote | hypothetical prote |        | hypothetical prote | hypothetical prote |        |        |        | hypothetical prote |          | _      |        |        | hypothetical prote | 88.6K hypothetical |

## ALIGNMENTS

RESULT 1 A42435

| Olly, T.M.  In from the salive modified  The from the salive modified  MATS  MATS  N 56 N 120  O2-Sep-2000  N.M.; Dudley, at forms a protection of the salive materials and the salive modified modified modified modified modified modified modifie |  | A5320  A5320  immunophilin FKBP46 - fall armyworm  C;Species: Spodoptera frugiperda (fall armyworm)  C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 0  C;Accession: A55320  R;Alnomri, E.S.; Fernandes-Alnemri, T.; Pomerenke, K.; Robertson,  J. Biol. Chem. 269, 30828-30834, 1994  A;Title: FKBP46, a novel Sf9 insect cell nuclear immunophilin tha  A;Reference number: A55320; MUID:95074110; PMID:7527037  A;Accession: A55320 | OCCE OY 5 DCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYN 56 1/1: : :         : : | Query Match 14.0%; Score 80.5; DB 2; Length 147; Best Local Similarity 32.7%; Pred. No. 1.7; Matches 18; Conservative 10; Mismatches 24; Indels 3; | elet A; residues: 59-91; DIO-LII3; 123-139 <con> (RBP4 F;1-21/Domain: signal sequence #status predicted <sig> (rote F;22-147/Product: leech antiplatelet protein #status predicted <mat></mat></sig></con> | J. Biol. Chem. 267, 6893-6898, 1992 A;Title: An inhibitor of collagen-stimulated platelet activation from the salivary gl. A;Reference number: A42434; MUID:92202246; PMID:1551897 A;Accession: A42434 A.McDischiot. | A;Cross-references: GB:M81489 A;Note: the authors translated the codon AGC for residue 20 as Arg and GAA for residue A;Note: the authors translation is shown at residue 65 A;Note: sequence extracted from NCBI backbone (NCBIN:91615) and modified R;Connolly, T.M.; Jacobs, J.W.; Condra, C. | C; Accession: A42435; A42434  R; Keller, P.M.; Schultz, L.D.; Condra, C.; Karczewski, J.; Connolly, T.M. J. Biol. Chem. 267, 6899-6904, 1992  A; Title: An inhibitor of collagen-stimulated platelet activation from the salivary gl A; Reference number: A42435; MUID:92202247; PMID:1551898 A; Accession: A42435 A; Molecule type: mRNA A; Residues: 1-147 < KEL> |
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C;Keywords: nucleus; phosphoprotein
F;324-371/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Experimental source: clone Y26D4A
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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δÃ
                                                                                                                                                                                                                      A; Cross-references: EMBL: 298877; PIDN: CAB11570.1; GSPDB: GN00023; CESP: Y69H2
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-907 <WIL>
                                                                                                                                                                                                                                                                                                                                                              R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Y69H2.2 - Caenorhabditis elegans
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                                                                                                                       A; Introns: 23/3; 65/1; 105/1; 146/1; 191/1; 241/1; 293/1; 381/1; 419/1; 461/1; 499/1;
                                                                                                                                                               A; Gene: CESP:Y69H2.2
                                                                                                                                                                                                 A; Experimental source: clone Y69H2
                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 CGNFLHNRPYPDSCETECMDTMVQVNAKPGPLMGSRNIKDNLTSSDECVKYCWKDLNCFV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 NYYDKDSKECWWWSIDNVHF-LEKVHPSEN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ANRKYTDFDKSFKKS-----SDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 VFEDTVNKECYYNVVDGEELDQEKFVVDEN 73
  10 YANRKYTDFDKSFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     госат
                                                             Local Similarity
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                                          33;
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                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; 25.6%;
                                                             13.7%; 29.2%;
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                                            12;
      ---KSSDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78.5;
Pred. No. 9.
                                                             Score 78.5; DB 2; Length 907; Pred. No. 16;
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                                              Mismatches
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                                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
      ---DECKKTC--FKTEYCYIVFEDT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 412;
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                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                              35;
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                                              Gaps
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                                              8
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A; Residues: 1-682 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                               밁
                                                                    Ωy
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                                                                                                                                                                                                              C; Genetics:
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                                                                                                                                                  Query Match
                                                                                                            Matches
                           382 ANEK--EYKKIIDKSDDRDDRDKDEYELE-----NEE--YNRDEEEDEGEDEEDE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
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                                                                      11 ANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYN----VVDGEELDQE 66
                                                                                                                                   Local
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Nucleic Acids Res. 28, 4317-4331, 2000, Aprille: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A; Reference number: A83650; MUID:20512582; PMID:11058132 A; Accession: B84021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B84021
                                                                                                                                                                                A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-797 < ALB>
A; Residues: 1-797 < ALB>
A; Residues: 1-797 < ALB>
A; Cross-references: GB:X64346; NID:g60320; PIDN:CAA45671.1; PID:g60369
A; Cross-references: GB:X64346; NID:g60320; PIDN:CAA45671.1; PID:g60369
A; Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, F
A; Tirol. 66, 5047-5058, 1992
A; Reference number: A37309; MUID:92333688; PMID:1321287
A; Contents: annotation; protein-coding frames
A; Note: neither protein nor nucleotide sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Albrecht, J.
submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus saimiri genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ORF48 - saimiriine herpesvirus 1 (strain 11)
C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 16-0ct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: chemotaxis protein cheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AP001517; GB:BA0000004; NID:g10175500; PIDN:BAB06689.1; GSPDB:GA;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two-component sensor histidine kinase involved in chemotaxis cheA [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A36806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 VNSRCI--VYEAGEME----TDPNACEDNSTLC-GAELGHGMCINWQSDVTD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 YAQEKSTD-DKTLKYLTLCGEWCMVSEDMLVKDDVSMKDDCKKSCGGDSSEYC----GK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 EELEEEKF -- DERFLYTLLTKVDGEE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 YDEFEMTVLDQSFEQGYQAYQIEVTLDE--KTLLKAARVFMVFEVLEQVG-EVIKSTPSA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 YANRKYTDFDKSFKKSSD-----LDECKKTCFKTEYCYIVFE--DTVNKECYYNVVDG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EELDQEKFVVDENFTENYLTDCEGKD 86
Conservative
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                              13.6%; Score 78; 32.3%; Pred. No.
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      12;
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                              DB
16;
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                                                                Length 797;
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      Indels
                                                                                                                                                                                                                                                                                                                                                              Biesinger, B.;
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          20;
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      Gaps
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A;Cross-references: EMBL:U00051; NID:g1216305; PID:g1216310; PIDN:AAA91358.1; CESP:F42G9A;Experimental source: strain Bristol N2 C;Genetics:
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A;Introns: 37/3; 254/2; 364/2; 406/2
                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-491 <TAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F42G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, March 1996 A; Description: The sequence of C. elegans cosmid F42G9.
                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: 218498
A; Accession: T16354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Taich,
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A;Introns: 57/3; 158/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F40G12.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T16354
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A;Residues: 1-264 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CESP:F40G12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: 277661; PIDN: CAB01183.1; GSPDB: GN00023; CESP: F40G12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, July 1996 A:Reference number: Z19507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F40G12.5 - Caenorhabditis elegans
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                  113 DIGDEG---
                                                                                                                                                              10 YANRKYTDF--DKSFKKSSDLDECKKTCFKTEYCYTVFEDTVNKECYYNVVDGEELDQEK 67
                                                                                               68 FVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD 101
                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 CFLEIVK-EECPEEKFKLIEENYSQLVTLLTE-KPKDNGACTAPYFQLEEIE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEREDCWTFYANRKYTDFDKSFKK-SSDLDECKKTCFKTEYCYIVFE-----DTVNKE 52
                                                                                                                                FTSAKLPDFLKERKFWEADDVAECLQKAF----VDFDDFIRAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYYNVVDGEELDQEKF-VVDENFTE--NYLTDCEGKDAGNAAGTGDESDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EESEDC-----FEKVFLAIISGKHECSK-----DYDFLARNLIQRREALTSGKE 72
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                                                                -KPKKAGGEADSEDEADRID 137
                                                                                                                                                                                                                        13.2%;
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                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                        Score 75.5;
Pred. No. 16
                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                        28;
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                                                                                                                                                                                                                                     Length 491;
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                                                                                                                                  -ESMKELK 112
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                                                                  PAR interacting protein - rat
C; Species: Rattus norvegicus (Norway rat)
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submitted to the EMBL Data Library, January 1997
                                  C; Accession: T32731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: ZK1290.10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-360 <TAI>
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                       P.A.;
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                  Ossipow, V.; Schibler,
                                                                                                                                                                                                                                                                                                                      Conservative
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33.3%;
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C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3844 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Barale, J.C.; Candelle, D.; Attal-Bonnefoy, G.; Dehoux, P.; Bonnefoy, S.; Ridley, Infect. Immun. 65, 3003-3010, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Y08926; NID:e1154302; PID:e311435; PIDN:CAA70130.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Plasmodium falciparum AARP1, a giant protein containing repeated motifs rich
A;Reference number: Z18929; MUID:97378065; PMID:9234746
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C;Superfamily: Caenorhabditis elegans hypothetical protein zK1290.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: The sequence of C. elegans cosmid ZK1290 A; Reference number: Z21535 A; Accession: T34510
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A;Experimental source: strain Bristol N2; clone ZK1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                      1786 K-KKNKKNVENQEKEFYVLNKIFVHNFI 1812
                                                                                                                                                                                                                                                                                                                                                                                   1726 EDSEECQIKESYKKMSECNNKENIIFDSISVLRKNNIKRLKNYMCKNKNCYIYYDDNNNK 1785
                                                                                                                                                                                                                                                                                                                      52 ECYYNVVDGEELDQEKFVVDENFTENYL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 EDTVGEE----NVFDFDKLFDKKIYIRNDGSTTENTTEQSTTEKTGTKKGTIEVSVELGEG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 EDTVNKECYYNVVDGEELDQEKFVV-----DENFTENYLTDCEGKDAGN-----AAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EEREDCWTFYANRKYTD-----FDK-SFKKSSDLDECKKTCFKTEYCYIVFEDTVNK 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%; Score 75; DB 2; 23.9%; Pred. No. 1.5e+02;
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A;Description: Isolation of PIP, a 160 kDa nucleolar protein that interacts with the act A;Reference number: Z21213
A;Reference number: T32731
A;Accession: T32731
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1277 <COM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein aq_1923 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70465
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                                                                                                                                                                                                                                                                          hypothetical protein BBH09 - Lyme disease spirochete plasmid H/lp28-3 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 C;Accession: B70236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain VF5
C;Genetics:
C;Genetics:
A;Gene: aq_1923
C;Superfamily: Aquifex aeolicus hypothetical protein aq_1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex acolicus
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70465
                                                       A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
A; Accession: B70236
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross_references: GB:AE000763;_NID:g2984178; PIDN:AAC07719.1; PID:g2984187; GB:AE00065
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                                                                                                                                                                                                                                 son,
                                                                                                                                                                                                                                                  R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
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                   A; Molecule type: DNA
A; Residues: 1-1278 <KLE>
                                                                                                                                                                                Nature 390,
A; Cross-references:
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                                                                                                                                                                                                              Bowman,
                                                                                                                                                                                   D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; wman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, re 390, 580-586, 1997
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    GB:AE000784; NID:g2690041;
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Pred. No. 53;
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  PIDN:AAC66000.1; PID:g2690056; TIGR:BBH09
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                                                  hypothetical protein F26F2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21428
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A; Residues: 1-4466 < OGA>
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                             R; Ainscough,
         submitted to the EMBL Data Library,
                                                                                                                                                   T21428
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Proc. Jpn. Acad. B Phys. Biol. Sci. 67, 27-31, 1991
A;Title: ATP-binding site in dynein beta-heavy chain: identification by molecular clo
A;Reference number: PSO415
A;Accession: PSO415
A;Accession: PSO415
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 764-1001, ApQ',1005-2036,'VPSSVET' <OG2>
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: ATP; heterotetramer; hydrolase; microtubule binding; nucleotide binding motif A (P-loop)
F;1852-1859/Region: nucleotide-binding motif A (P-loop)
F;2805-2812/Region: nucleotide-binding motif A (P-loop)
F;1807-2813/Region: nucleotide-binding motif A (P-loop)
F;1807-2813/Region: nucleotide-binding motif A (P-loop)
F;1808/Binding site: ATP (Lys) *status predicted
F;2139/Binding site: ATP (Lys) *status predicted
F;2466/Binding site: ATP (Lys) *status predicted
F;2466/Binding site: ATP (Lys) *status predicted
F;2481/Binding site: ATP (Lys) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dynein beta heavy chain, ciliary - sea urchin (Anthocidaris crassispina)
N;Contains: dynein ATPase (EC 3.6.4.2)
C;Species: Anthocidaris crassispina
C;Date: 30-Sep-1991 #sequence_revision 02-May-1994 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Four ATP-binding sites in the midregion of the beta A;Reference number: S17231; MUID:91326104; PMID:1830928 A;Accession: S17231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:D01021; NID:g217202; PIDN:BAA00827.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 YGEKRYIEFD--FSKIKEKEE-----YKEQEWFILFSYLIRKERYLKTSNIISVEKEQIS 233
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                                                                                                                                                 460 EEFQECAKVFTERPYDGLDPTCQEFLEDYEEFEKKVFDLDRRLGSILCQGFDDCCGLEAA 519
                                                                    36 FKTEYCY-----IVFEDTVNKECYYNVV---DGEELDQEKFVVDEN 73
                                                                                                                                                                                                                          1 EEREDCWTFYANRKY-----KTC 35
FKMLDCYGPLLDRPVIRNDF---ECKYPIVLMLYDQELDQSKEIYDEH 564
                                                                                                                                                                                                                                                                                                           14;
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Pred. No. 2.1e+0;
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A;Reference number: Z19420
A;Reference number: Z19420
A;Recession: T21428
A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Accession: T21428
A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Accession: T2043 (WIL)
A;Cross: references: EMBL:Z81514; PIDN:CAB04192.1; GSPDB:GN00023; CESP:F26F2.6
A;Experimental source: clone F26F2
C;Genetics:
A;Gene: CESP:F26F2.6
A;Introns: 18/3; 116/3; 142/1; 265/3; 306/3; 373/3; 403/2; 425/2; 479/3; 544/3; 573/2;
A;Gene: CESP:F26F2.6
A;Introns: 18/3; 116/3; 142/1; 265/3; 306/3; 373/3; 403/2; 425/2; 479/3; 544/3; 573/2;
A;Gene: CESP:F26F2.6
A;Introns: 18/3; 116/3; 142/1; 265/3; 306/3; 373/3; 403/2; 425/2; 479/3; 544/3; 573/2;
A;Gene: CESP:F26F2.6
A;Introns: 18/3; 116/3; 142/1; 265/3; 306/3; 373/3; 403/2; 425/2; 479/3; 544/3; 573/2;
A;Gene: CESP:F26F2.6
A;Map position: 5
A;Introns: 18/3; 116/3; 142/1; 265/3; 306/3; 373/3; 403/2; 425/2; 479/3; 544/3; 573/2;
A;Gene: CESP:F26F2.6
A;Map position: 5
A;Introns: 18/3; 116/3; 142/1; 265/3; 306/3; 373/3; 403/2; 425/2; 479/3; 544/3; 573/2;
A;Gene: CESP:F26F2.6
A;Map position: 5
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PS12_ARATH
D7_AEDAE
SPT8_YEAST
RRPP_PIRYV
CC45_YEAST
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CALX_RAT
YJO8_YEAST
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| RESU<br>FKB4<br>ID<br>AC                | Qy<br>Db  | S FT FT                                     | 888888888  | 48888  |   | 2 0 0 0 0 S   |  | RESULT<br>LAPP_H<br>ID L |            |  |      |
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| RESULT 2 FKB4_SPOFR ID FKB4_S AC Q26486 | Matches y 4 b 65  | SIGNAL CHAIN SEQUENCE SEQUENCE              | This SWI between the Eurouse by modified entities or send from Signal  |  | SEQU<br>TISS<br>MEDL<br>Kell<br>"An<br>sali   | Haem<br>Euka<br>Rhyn<br>NCBI  | O1-FE<br>O1-FE<br>O1-FE<br>Anti-   | JLT 1<br>HAEOF<br>LAPP_  |            | 00000000000000000000000000000000000000   | 34   |
| T 2 SPOFR FKB4_SPOFR D26486;            |   | ENCE  | th<br>th<br>no<br>an<br>rea<br>rea<br>148  | tiol. Chem. 267:6899-6 FUNCTION: AN INHIBITO AGGREGATION, DENSE GR SUBCELLULAR LOCATION: | SEQUENCE FROM N.A., AND TISSUE=Salivary gland; MEDLINE=92202247; PubMe Reller P.M., Schultz L. "An inhibitor of collag salivary glands of the the cDNA and expression | nteri<br>yota;<br>hobde<br>TaxID  | 01-FEB-1994 (Rel<br>01-FEB-1994 (Rel<br>01-FEB-1994 (Rel<br>Anti-platelet pr | F<br>_HAEOF<br>47:       |            |  | 66.5 |
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| STANDARD;                               | vative DFDKSFF  | 21<br>147<br>15908<br>14.9%                 | wiss Institution institution formati institution formati institution institution in to licen il to licen AAA29194.1; | :6899-6<br>NHIBITO<br>ENSE GR  | N.A., AND S ry gland; 247; PubMed= Schultz L.D. Sof collagen ds of the Ha expression."  | a officinalis (Mexican<br>Metazoa; Annelida; Cl<br>Ilida; Glossiphoniidae<br>=6410; |  | STANDARD;                |            | 1447<br>1647<br>165<br>428<br>428<br>455<br>725<br>746<br>793<br>1124<br>1124<br>11281   | 1033 |
| ν<br>+                                  | CKS   |   | co<br>cut<br>cit<br>cit  | RAN<br>S   | SEQ   | (Me<br>Lid<br>ion   | eat<br>st  |                          |            |  | مبر  |
| PRT; 412 AA.                            | י מע  | ELET<br>874A4                               | yright. It is pro of Bioinformatic Institute. There tions as long as is not removed. agreement (See ht isb-sib.ch).  |  | UENCE OF 60-91 ANI<br>51898;<br>Condra C., Karczew<br>timulated platelet  | leech).<br>itellata;<br>; Haemente  | Created) Last sequence update) Last annotation update) precursor.            | PRT; 147 AA.             | ALIGNMENTS | CB20 XENIA CB20 XENIA ADEL_SCHPO ADEL_CAEEL RF4_KUULA YNU6_YEAST YNU6_YEAST GYP7_YEAST NETB_DROWE TCF8_HUMAN TRPS_HUMAN TRPS_HUMAN TRPS_HUMAN  |      |
|   | 24; Indels 3; Gaps CYIVFEDTVNKECYYN 56     :       CYILQINTETNECYRN 120 | PROTEIN.<br>E42E CRC64;<br>B 1; Length 147; | through a collabor d the EMBL outstat no restrictions on content is in no by and for comme www.isb-sib.ch/anno       | STIMULATED PLATELET<br>AND SEROTONIN RELEASE.  | ) 123-139.  ### ### ### ### #### ###############  | Hirudinida; Hirudinea;<br>ria.  |  |                          |            | P52299 xenopus lae P52299 xenopus lae Q10435 schizosacch Q07750 caenorhabdi P08806 kluyveromyc P40161 saccharomyc P50640 mycobacteri P48365 saccharomyc Q24568 drosophila P37275 homo sapien Q9uhf7 homo sapien P55155 caenorhabdi |      |
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RESULT 3
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14)Ppothetical gene 4
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"FKBP46, a novel Sf9 insect cell nuclear immunophilin that forms a protein-kinase complex.";
J. Biol. Chem. 269:30828-30834(1994).
- FUNCTION: BINDS TO, AND IS INHIBITED BY FK506 AND RAPAMYCIN. BINDS DOUBLE-STRANDED DNA IN VITRO. PPIASES ACCELERATE PROTEIN FOLDING.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isomerase) (PPiase) (EC 5.2.1.8).

Spodoptera frugiperda (Fall armyworm).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;

Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; (
Ditrysia; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                           Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage;
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              Gammaherpesvirinae;
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HSSP; P20071; 1FKJ.
InterPro; IPR001179; FKBP_PPIase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95074110; PubMed=7527037; Alnemri E.S., Fernandes-Alnemri T.,
NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00254; FKBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-trans isomerase) (PPiase) (EC 5.2.1.8).
                                                                                                                                                                                                                                     175
                                                                                                                                                                                                                                                                                                 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   somerase;
                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                              11 ANRKYTDFDKSFKKS-----SDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear KINASE IN THE PRESENCE OF MG2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                     DE--NDESFKMN--TSAEGDDSDEEDDDDEDEEDDDD 208
                                                                                                                                                                                                                                                                 EKFYVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                               ANKKAKPDKKAGKNSAPAAESDSDDDD-
                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00454; FKBP_PPIASE_2; PS50059; FKBP_PPIASE_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00453; FKBP_PPIASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                     ;; Rotamase; Nuclear p
91 112 1
120 145 1
152 216 2
152 216 2
152 219 1
219 219 1
324 412 AA; 45810 MW;
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                       STANDARD;
                                                                          25, Created)
25, Last sequence update)
25, Last annotation update)
48 protein.
              Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                          14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                        WW;
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                                                                                                                                                                                                                                                                                                                                                         Score 80.5; DI Pred. No. 1.7; L2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    PPIASE, FKBP-TYPE. F2A69159AEF4FE22
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYS-RICH (BASIC).
ASP/GLU-RICH (HIGHLY ACIDIC).
LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; DNA-binding; Phosphorylation
ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALSE_NEG.
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                                                                                                                                                       797
                             Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                              EDQLQK----FLDGEDIDT 17
                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Length 412;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robertson N.M.,
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                                                                                                                                                                                                                                                                                                                                                           27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          commercial
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RESULT 4
ICEC_MOUSE
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Best Local :
                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                            Fiers W.;
"Characterization of seven murine caspase family members.";
FEBS Lett. 403:61-69(1997).
-!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
15-JUN-2002 (Rel. 41, Last ann
Caspase-12 precursor (EC 3.4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                             wan de Craen M., Vandenabeele P., Declercq W.,
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICEC_MOUSE 008736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                          STRAIN-C3H/An;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                       CASP12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 7
                                                                                                                                                                                                                                                                            van Loo G., Molemans F., Schotte P., van Criekinge W., Beyaert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A36811; A36811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X64346; CAA45671.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92333688; PubMed=1321287;
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                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO EBV BRRF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 KDEKEEGEDEGDDGEDEGEDEGE--DEGDEGDEGDE 461
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                                                                                                                                  RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY).
SUBUNIT: HETERODIMER OF TWO SUBUNITS (POTENTIAL).
TISSUE SPECIFICITY: MAINLY EXPRESSED IN SKELETAL MUSCLE AND LUNG
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDE 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88867 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Last sequence update), Last annotation updat (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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M A., Coleman F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                          restrictions
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                                                                                          EMBL outstation
                                                                                                          a collaboration
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s requires a license agreement (See http://www.isb-sib.ch/announce/ an email to license@isb-sib.ch).

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PROSITE; PS01121; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1312922; Casp12.
InterPro; IPR001315; CARD.
InterPro; IPR002338; ICE_D10.
InterPro; IPR002338; ICE_D10.
InterPro; IPR001309; ICE_P20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y13090; CAA73532.1; -. HSSP; P29466; lICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C14.01
                                                                                                                                                                                                                                                                                                                                                                                                                       P2C1_CAI
P49595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-RVV-1997 (Rel. 35, Last annotation update)
Probable protein phosphatase 2C F42G9.1 (EC 3
                                                                                                                                                                                           Taich A., Waterston R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                F42G9.
                                                                                                                                          phosphate.
-!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239
EMBL; U00051; AAA91358.1; -.
                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 VFEDTVNKECYYNVVDGEEL----DQEKEVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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1 ? POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47853 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B94B0FED16B1CB40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            491 AA.
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                                                                                                                                                                                                                                                                                                                                                                   3.1.3.16) (PP2C).
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                                                                                 Query Match
Best Local Similarity
                                                                   Matches
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METAL 37 37 MANGANESE 1 (BY SIMILARITY).

METAL 38 MANGANESE 1 (BY SIMILARITY).

METAL 57 57 MANGANESE 1 AND 2 (BY SIMILARITY).

METAL 428 428 MANGANESE 2 (BY SIMILARITY).

METAL 477 477 MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00481; PP2C; 1.
SMART; SM00331; PP2C_SIG; 1.
SMART; SM00332; PP2CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WormPep; F42G9.1; CE07231.
InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
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                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 39.7 kDa protein ZK1290.10 in chromosome II precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q09337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 DIGDEG------KPKKAGGEADSEDEADRID 137
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZK1290.10
                                                                                                                                                             Hypothetical protein; Signal.
                                                                                                                                                                                                EMBL; U21308; AAB93316.1; --
WormPep; ZK1290.10; CE02080.
InterPro; IPR003582; ShKT.
SMART; SM00254; ShKT; 1.
                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 YANRKYTDF--DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDOEK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 FTSAKLPDFLKERKFWEADDVAECLQKAF-----VDFDDFTRAE------ESMKELK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
224 EDTVGEE----NVFDFDKLFDKKIYIRNDGSTTENTTEQSTTEKTGTKKGTIEVSVELGEG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 FVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD 101
                               46 EDTVNKECYYNVVDGEELDQEKFVV-----DENFTENYLTDCEGKDAGN-----AAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAEEL
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                                                                                                                                     360 AA;
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                                                                   Conservative
                                                                                                                                                   22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CE07231.
                                                                                                                                   360 F
39669 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 75.5; Di
24.5%; Pred. No. 5.9;
                                                                                   13.1%; Score 75; DB 1; Length 360; 33.3%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                       9; Mismatches
                                                                                                                                   HYPOTHETICAL PROTEIN ZK1290.10.; 18751B6BC062D4F7 CRC64;
                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                        23;
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                                                                          Indels
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                                                                            14; Gaps
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95 DESDEVDED 103

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RESULT 8
DYNC_ANTCR
ID DYNC_A
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DT 01-FEB
DT 01-FEB
DT 30-MAY
DE DYNCHO
OC Eukary
OC Eukary
OC Eukary
OC Anthoc
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OX NCBL_T
RN [1]
RP SEQUEN
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                                                                                                                                                                                                                                       DYHC_ANTCR STANDARD; PRT; 4466 AA. P39057; Ol-FEB-1995 (Rel. 31, Created) Ol-FEB-1995 (Rel. 31, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Dynein beta chain, cillary.
                                                                                                                                                      Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinodea; Echinoidea; Echinodea; E
                                                                                                                                                                                                                  Anthocidaris crassispina (Sea urchin)
   Ogawa K.;
                                                         SEQUENCE FROM N.A.
                                                                                                                                          Anthocidaris.
                     MEDLINE=91326104; PubMed=1830928;
                                                                                                            NCBI_TaxID=7629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000763; AAC07719.1; -.
Hypothetical protein; Signal; Complete proteome.
SIGNAL 1 20 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
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16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 FYANRKYTD-----FDKSFKKSSDLDECKKTCFKTEYCYIVFE----DTVNKECY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNVVDGEELDQEKFVVDENFTENYLTDCEGK 85
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(Rel. 40,
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24.2%;
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Last annotation update
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Pred. No.
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  Damagnez V., Tillit J., de Recondo A.-M.,
                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                          DPOA_SCHPO STANDARD; PRT; 1405 AA. P28040; O1-AUG-1992 (Rel. 23, Created) O1-AUG-1992 (Rel. 23, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                      SEQUENCE FROM N.A.
MEDLINE=91238692; PubMed=2034212;
                                                                                                                                                                                                                                                                                                                                                                                                                     SCHPO
                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                      DNA polymerase alpha catalytic subunit (EC 2.7.7.7) (DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
SEQUENCE
                                                                                                    NCBI_TaxID=4896
                                                                                                                                                                                                                      POL1 OR SWI7 OR SPAC3H5.06C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 EEFQECAKVFTERPYDGLDPTCQEFLEDYEEFEKKVFDLDRRLGSILCQGFDDCCGLEAA 519
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Pfam; PF03028; Dynein_heavy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S17231; S1723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D01021; BAA00827.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THREE INTERMEDIATE CHAINS AND SEVERAL LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 FKTEYCY-----IVFEDTVNKECYYNVV---DGEELDQEKFVVDEN 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FKMLDCYGPLLDRPVIRNDF---ECKYPIVLMLYDQELDQSKEIYDEH 564
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SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS (ALPHA AND BETA),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                                                                                                 Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dynein; ATP-binding; Flagella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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Baldacci G.;
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RX MEDLINE—21848401; PubMed=11859360;
RX MEDLINE—21848401; PubMed=11859360;
RA WOOd V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA WOOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Bowman S.,
RA Syouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher G.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feitwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gollins M., Connor R., Cronin A., Leather S., McDonald S., McLean J.,
RA Gollins M., Connor R., Fertz G., Walsh M.A., Rabbinowitsch E.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., More K., Hurst S.M.,
RA Galibert F., Starbert M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Galibert F., Bender M., Galibert M., Gali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The POL1 gene from the fission yeast, Schizosaccharomyces pombe, shows conserved amino acid blocks specific for eukaryotic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93140876; PubMed-8423854; Jagmohan S., Klar A.J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerases alpha."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 361:271-273(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA polymerase-alpha is essential for mating-type switching in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                 EMBL; X58299; CAA41232.1; --
EMBL; X69673; CAB57881.1; --
EMBL; Z99296; CAB16598.1; --
PIR; S15993; DJZPA.
                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                  Pfam; PF00136; DNA_DOL_B; 1.
Pfam; PF03104; DNA_DOL_B_exo; 1.
PRINTS; PR00106; DNAPOLB.
SMART; SM00486; POLBC; 1.
DNA-binding; Nuclear protein.
                       TIGREAMS; TIGRO0592; pol2; 1.

PROSITE; PS00116; DNA_POLYMERASE_B; 1.

Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                    InterPro; IPR002064; DNA_pol_B. InterPro; IPR004578; Pol2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES: ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE DIFFERENT REACTIONS OF DNA SYNTHESIS.
SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPLICATIVE POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yeast.".
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SS
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YNV2_YEAST
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                                                           RESULT 11
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 88.8 kDa protein in PEX17-MER1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P40157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNV2_YEAST
                                                                                                                                                                                                                                                                                                                                                              use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288C / FY1679;
MEDLINE-95282517; PubMed=7762305;
Coster F., van Dyck L., Jonniaux J.-L., Purnelle B., Goffeau A.;
The sequence of a 13.5 kb DNA segment from the left arm of yeast
Chromosome XIV reveals MERI; RAPI; a new putative member of the DNA
chromosome XIV reveals MERI; RAPI; a new putative member of the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replication complex and a new putative serine/threonine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 FEDTVNKECYYNVVDGE-----ELDQEKFVVDEN---FTENYLTDCEGKDAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 YESKENEELYDNVSEEEYRKIVRORLDEDDFVVDDNGAGYVDN-----GYDEWDQSHYS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast 11:85-91(1995)
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                                                                                                                                                                                                                                                                                                                        EMBL; X78898; CAA55496.1; --
EMBL; Z71488; CAA96114.1; --
SGD; S0005156; YNL212W.
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                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 782 AA; 88845 MW; CCBB1F4CE32BF97C CRC64;
p81034;
15-JUL-1998 (Rel. 36, Created)
                               MOH1
                                                CANPG
                                                                                                                                                                    315 KFKDLDKCIQFRFAMVKCLMM----TLNKETWTDVPEKEKDYILDSSSVPLEKQFDDILHI 371
                                                                                                          372 DDRSNEERDKESSESENDSEDED 394
                                                                                                                                        81 DCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                  24 KSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEE---LDQEKFVVDENFTENYLT 80
                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO C.CARDUNCULUS PROTEIN CYPRO4 AND S.POMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPBC1685.14C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                               CANPG
                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                     Conservative
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                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159348 MW; 06082A3BAD6347C2 CRC64;
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                                                                                                                                                                                                                                                          12.4%; Score 71; DB
                                                                                                                                                                                                                                                       26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                       Pred. No.
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                                         78 AA.
                                                                                                                                                                                                                                                                         DB 1; Length 782;
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PA21_CANFA
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                             MEDLINE=90306027; PubMed=2142076;
Kerfelec B., Laforge K.S., Vasiloudes
"Isolation and sequence of the canine
                                                                                             "Dog and rat pancreatic phospholipases A2: complete amino acid sequences deduced from complementary DNAs.";
J. Blochem. 99:733-739(1986).
Eur. J. Biochem. 190:299-304(1990).
                            gene.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                           Eukaryota; Metazoa; Choruata; Camidae; Fissipedia; Canidae;
                                                                                                                                             Ohara O., Tamaki M., Na.
Teraoka H., Okamoto M.;
                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine
                                                                                                                                                                     MEDLINE=86223862; PubMed=3754861;
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              acylhydrolase) (Group IB phospholipase A2).
                                                                                                                                                                                                                                                           Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                            P06596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuropeptide; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Mandibular organ-inhibiting hormone-1 (MOIH-1).
Cancer pagurus (Rock crab).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Malacostraca; Eubrachyura; Cancroidea; Cancridae; Cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01147; Crust_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wainwright G., Webster S.G., Wilkinson M.C., Chung J.S., Rees H.H., "Structure and significance of mandibular organ-inhibiting hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Sinus gland;
MEDLINE-96278659; PubMed-8662685;
                                                                                                                                                                                                                                                                                                                                                                                                                          6 DCONFIGNRAMYEKVDWICKDCANIFRKDGLLNNCRSNCFYNTEFLWCIDATENTRNKE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 DCWIFYANRKY------TDFDKSFKKSSDLDECKKTCF-KTEY--CYIVFEDTVNKE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                                                                                                      CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wth and reproduction.",

Biol. (Chem. 271:12749-12754(1996).

FUNCTION: REPRESSES THE SYNTHESIS OF METHYL FARNESOATE, THE PRECURSOR OF INSECT JUVENILE HORMONE ILI IN THE MANDIBULAR ORGAN.

TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN.

TISSUE SPECIFICITY: PRODUCED BY THE MEDULA TERMINALIS X-ORGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE ARTHROPOD CHH/MIH/GIH/VIH FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE EYESTALKS AND TRANSPORTED TO THE SINUS GLAND WHERE IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001166; CHH_MIH_GIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer pagurus. Involvement in multihormonal regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9241 MW;
                                                                                                                                             Nakamura E., Tsuruta Y., Fujii Y., Shin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _neurohorm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8DB338A39058A62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
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                       pancreatic phospholipase
                                                                                                                                                                                                                                                                                                                                                                 146 AA
                                       Puigserver A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                       Euteleostomi;
Canis.
                                    Scheele G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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CB20_HUMAN
                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                                    Query Match
                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
20 kDa nuclear cap binding protein (NCBP 20
            interacting protein 1) (NIPi). NCBP2 OR CBP20.
Homo sapiens (Human).
                                                                                          P52298; Q14924;
                                                                                                           CB20_HUMAN
                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                CA_BIND
                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Lipid degradation; Calcium; Pancreas; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00118; PA2_HIS; PROSITE; PS00119; PA2_ASP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00068; phoslip;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M35301; AAA30883.1; -. PIR; A24392; PSDG. PIR; S11316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                         60 VDELDKCCQTHDHCY-----SEAKKLDSCKFLLDNPYTKIYSYSCSGSE 103
                                                                                                                                                                                  28 LDECKKTCFKTBYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00085; PA2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001211; PhospholipaseA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-8175472; PubMed=3562437;
Kerfelec B., Laforge K.S., Puigserver A., Scheele G.A.;
"Primary structures of canine pancreatic lipase and phospholipase A2
messenger RNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of 2-acyl groups in 3-sn-phosphoglycerides.
-i- CATALYTIC ACTIVITY: PhosphatidyLcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pancreas 1:430-437(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acylglycerophosphocholine + a fatty acid anion. COFACTOR: Binds 1 calcium ion per subunit (By similarity).
                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D00035; BAA00023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P00592; 4P2P
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                          146 AA;
                                                                                                                                                                                                                       Conservative
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                    146
67
127
120
113
118
50
52
                                                                                                                                                                                                                                                                          16235 MW;
                                                                                                                                                                                                                                 12.3%; Score 70.5; D
25.4%; Pred. No. 4.9;
                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        PHOSPHOLIPASE A2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                       BY SIMILARITY.

VIA CARBONYL OXYGEN (BY SIMILARITY).

VIA CARBONYL OXYGEN (BY SIMILARITY).

VIA CARBONYL OXYGEN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                 F6258ED9527F3692 CRC64;
                                                                                                 156 AA
                                              update)
                                                                                                                                                                                                                                            DB 1;
                          kDa subunit) (CBP20) (NCBP
                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                         Length 146;
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                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local
- METJA
7875.METJA STANDARD; PRT; 748 AA
Q58285;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                           Nuclear protein; RNA-binding.

DOWAIN 40 118 RNA-BINDING (RRM).

CONFLICT 97 97 A -> S (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-stb.ch/announce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             мім; 605133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D59253; BAA09599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X84157; CAA58962.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: INVOLVED IN MEDIATING U SNRNA EXPORT FROM THE NUCLEUS.
BINDS TO 5'CAPPED MRNA.
-!- SUBUNIT: THE CAP-BINDING PROTEIN (CBC) COMPLEX IS AN HETERODIMER
OF CBP80 AND CBP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kataoka N., Ohno M., Moda I., Shimura Y.; "Identification of the factors that interact with NCBP, an 80 kDa nuclear cap binding protein."; Nucleic Acids Res. 23:3638-3641(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Cervix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Cervical carcinoma;
MEDLINE-96017765; PubMed-7478990;
                                                                                                                                            88
                                                                                                                                                         45 FEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A cap-binding protein complex mediating U snRNA export.";
Nature 376:709-712(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 9-25 AND 113-145 MEDLINE-95379956; PubMed=7651522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McGuigan C., Mattaj A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Izaurralde E., Lewis J., Gamberi C., Jarmolowski A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
                                                                                                                                                                                                                        1 EERE-----DCWTFYANRKYTDFDKS----FKKSSD------LDECKKTCFKTEYCYIV 44
                                                                                                                           YYSRADAENAMRYINGTRLDDR--IIRTDWDAGFK---EGRQYGRGRSGGQVRDEYRQD 141
                                                                                                                                                                                          EEQEKLLKKSCTLYVGNLSFYTTEEQIYELFSKSGDIKKIIMGLDKMKKTA--CGFCFVE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC001255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:7659; NCBP2.
                                                                                                                                                                                                                                                                             h 12.3%; Score 70.5; D
Similarity 21.8%; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                          156 AA; 18001 MW; B6C94F3182A2CC3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH01255.1; -.
                                                                                                                                                                                                                                                           20; Mismatches
                                                    748 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                        DB 1; Length 156;
                                                                                                                                                                                                                                                           50; Indels
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S185_YEAST
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STRAIN-S288c;
                                                                        "The SAP, a new family of proteins, associate and function positively with the SIT4 phosphatase."; Mol. Cell. Biol. 16:2744-2755(1996).
                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SIT4-associating protein SAP185.
SAP185 OR YJLL098W OR J0840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S185_YEAST
P40856;
                                                                                                                                                                                                 Luke M.M., della Seta F., di Como C.J., Sugimoto H., Kobayashi R.,
                           SEQUENCE FROM N.A.
                                                                                                                                                                                          Arndt K.T.;
                                                                                                                                                                                                                                                  MEDLINE=96220458; PubMed=8649382;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.
SEQUENCE 748 AA; 90731 MW; 5515ED3B541562EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67531; AAB98882.1; -. TIGR; MJ0875; -.
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Gverbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.G.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 KKAEIFNKHFYYNLM-----AQKFESERKFKE-----AAEYYKKSGDTIKEIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 KEFSDIWMYFDIKIYYYKKLSIKHRKFEGNLDKAIELTE---KCYKLAEESYNKFNDKNY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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Hypothetical protein MJ0875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 ----TVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDE 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 70.5;
24.4%; Pred. No. 27
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Search completed: February 25, 2003, 02:31:32 Job time : 15 secs
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3 genes, a TCP-1-related gene, an open reading frame similar to the DAL80 gene, and a tRNA(Arg)."; yeast 11:873-883(1995).

Teast 11:873-883(1995).

PUNCTION: ASSOCIATES WITH THE SIT4 PHOSPHATASE IN A CELL CYCLE DEPENDENT MANNER. MAY BE DIRECTLY OR INDIRECTLY INVOLVED IN SIT4-DEPENDENT FUNCTIONS IN BUDDING AND IN NORMAL G1 CYCLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence and function analysis of a 9.74 kb fragment of Saccharomyces cerevisiae chromosome X including the BCK1 gene."; yeast 10:1481-1488(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95176706; PubMed-7871887; Miosga T., Boles E., Schaaff-Gerstenschlaeger I., Schmitt S., Zimmermann F.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-853 FROM N.A.
STRAIN-S288c / FY1679;
MEDLINE-96090136; PubMed=7483851;
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X77923; CAA54892.1; -. EMBL; X85021; CAA59396.1; -. EMBL; Z49373; CAA89392.1; -. SGD; S0003634; SAP185.
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation; Cell cycle.
SEQUENCE 1058 AA; 121402 MW; DD44DD53DDD87438 CRC64;
                                                                              542 EDD 544
                                                                                                                   101 DED 103
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                                                                                                                                                                                                                                                                                                              12.2%; Score 70; DB 1; Length 1058; 20.3%; Pred. No. 43; tive 27; Mismatches 45; Indels
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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573
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SUMMARIES
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| 4.5                | 44                 | 43                 | 42     | 41                 | 40                | 39                | 38     | 37                 | 36     | 35     | 34     | ω<br>ω | 32                 | 31     | 30                 | 29                 | 28     | 27                 | 26                 | 25                 | 24                | 23                 | 22                | 21     | 20     | 19     | 18                 | 17                |
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| 70                 | 70                 | 70                 | 70     | 70                 | 70                | 70                | 70     | 70                 | 70.5   | 70.5   | 70.5   | 70.5   | 70.5               | 70.5   | 70.5               | 71                 | 71     | 71                 | 71.5               | 71.5               | 71.5              | 72                 | 72.5              | 72.5   | 72.5   | 73     | 73                 | 73.5              |
| 12.2               |                    |                    |        | 12.2               |                   |                   |        |                    |        |        |        |        |                    | 12.3   | 12.3               | 12.4               | 12.4   | 12.4               | 12.5               | 12.5               | 12.5              | 12.6               | 12.7              | 12.7   | 12.7   | 12.7   | 12.7               | 12.8              |
| 1481               | 1255               | 1167               | 793    | 703                | 669               | 521               | 328    | 292                | 2472   | 786    | 600    | 367    | 296                | 256    | 112                | 851                | 589    | 551                | 594                | 540                | 320               | 1303               | 2533              | 2533   | 564    | 2543   | 643                | 1154              |
| ر.<br>د            | 16                 | 16                 | 10     | 10                 | Çī                | Çī                | σ      | 12                 | ហ      | 10     | 16     | G      | 11                 | 10     | U                  | 4                  | 4      | 4                  | 16                 | 16                 | σı                | 10                 | σı                | U      | ഗ      | G      | σ                  | Çī                |
| Q9NEX0             | Q97116             | Q9ZLG7             | Q9SPU5 | Q9LKR9             | Q8SXS8            | Q94718            | Q22144 | Q65239             | Q8T2M5 | Q9C7E7 | Q8RHS6 | Q9VIR9 | Q9D5G6             | Q9CA59 | Q9U5Y6             | Q9H501             | Q9HA35 | Q9NX93             | Q9PP61             | Q8XHG9             | 096214            | Q9SKS0             | P90589            | Q27183 | 001627 | P90649 | Q9XV53             | Q9V6S9            |
| Q9nex0 caenornabdi | Q97ii6 clostridium | Q9zlg7 helicobacte |        | Q9lkr9 arabidopsis | Q8sxs8 drosophila | Q94718 paramecium |        | Q65239 african swi |        | ~      |        |        | Q9d5g6 mus musculu | 9      | Q9u5y6 cancer pagu | Q9h501 homo sapien |        | Q9nx93 homo sapien | Q9pp61 campylobact | Q8xhg9 clostridium | O96214 plasmodium | Q9sks0 arabidopsis | P90589 paramecium |        |        |        | Q9xv53 caenorhabdi | Q9v6s9 drosophila |

## ALIGNMENTS

| QY 36 FKTEYCYIVFEDT                   | Qy 10 YANRKYTDFDKSF<br>       :  :<br>Db 11 YNTRNYSDAINYY | Query Match  Best Local Similarity 22.  Matches 22; Conservative                                      | KW Hypothetical protein; Complete SQ SEQUENCE 116 AA; 13590 MW; | InterP |                                | RT flesh-eater."; |                   | RA FubMeu-11/92042; RA Shimizu T., Ohtani  | RC STRAIN=13 / TYPE A; | OX NCBI_TaxID=1502; | OS CIOSTIGIUM PETITINGENS: Ba   | ical             | DT 01-JUN-2002 (TremBirel.       | 01-MAR-2002 ( | <pre>ID Q8xJ41 PRELIMINARY;</pre> | RESULT 1<br>Q8XJ41 |
|---------------------------------------|---|---|---|--------|--------------------------------|-------------------|-------------------|--|------------------------|---------------------|---|------------------|----------------------------------|---------------|-----------------------------------|--------------------|
| FKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFV 69 | YANRKYTDFDKSFKKSSDLDECK                                   | 13.7%; Score 78.5; DB 16; Length 116; 22.7%; Pred. No. 1.9; vative 11; Mismatches 27; Indels 37; Gaps | 13590 MW; 9D6B5D847B3A7312 CRC64;                               | PR.    | sci. U.S.A. 99:996-1001(2002). | CE OT C           | Kuhara S., Hayash | K., Hirakawa H., Ohshima K., Yamashita A., |                        |                     | Clostriqium pertringens.<br>Bacteria: Firmicutes: Bacillus/Clostridium group; Clostridia; | protein CPE1920. | rel. 21, Last annotation update) | 20, Creat     | INARY; PRT; 116 AA.               |                    |

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FNLAYCYSMINNNSKALRYFNLAWALDNADIDCEKAI 107

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RESULT 3
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Q9U2Q4;
Q9U2Q4;
Q1-MAY-2000 (TIEMBLrel. 13, Cr
\(\cappa_may-2000\) (TIEMBLrel. 13, Lr
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Q9X9S1;
Q1-NOV-1999
                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae;
                                                                                               SEQUENCE
                                                                                                                     SMART;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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"A single gene (tts) located outside the cap locus directs the formation of Streptococcus pneumoniae type 37 capsular polysacc type 37 pneumococci are natural, genetically binary strains.";

J. Exp. Med. 19:241-251(1999).

EMBL; AJ131985; CAB51329.1; -.

InterPro; IPR001173; Glycos_transf_2.

Pfam: PF00535; Glycos_transf_2; 1.

SEQUENCE 509 AA; 58888 MW; C6C38D2ACFABOD8A CRC64;
                                                                                                                   InterPro; IPR001304; Lectin_C.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Bacteria; Firmicutes; Bacillus/Clostridium
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01-DEC-2001
                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans:
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    L Similarity
23; Conser
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    Conservative
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Best Local
                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last anotation update)
Two-component sensor histidine kinase involved in c.
                                                                                                                    01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF_1; UNKNOWN_8.
PROSITE; PS01186; EGF_2; 4.
EGF-1ike domain; Glycoprotein.
SEQUENCE 907 AA; 101840 MW; 8B5
  Bacteria; Firmicutes;
                      Bacillus halodurans
                                                 CHEA OR BH2970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00858; ASC; Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 298877; CAB11570.1; HSSP; Q12784; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MCMUTTAY A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9XTS9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XTS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y69H2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y69H2.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                               280
                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 NYYDKDSKECWWWSIDNVHF-LEKVHPSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 YANRKYTDFDKSFK------KSSDL------DECKKTC--FKTEYCYIVFEDT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 VFEDTVNKECYYNVVDGEELDQEKFVVDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                        YAQEKSTD-DKTLKYLTLCGEWCMVSEDMLVKDDVSMKDDCKKSCGGDSSEYC----GK
                                                                                                                                                                                                                                                                                                             VNSRCI--VYEAGEME-----TDPNACEDNSTLC-GAELGHGMCINWQSDVTD
                                                                                                                                                                                                                                                                                                                                                       VNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000561; EGF-like. IPR001438; EGF_II.
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Na+channel_ASC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the
Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12,
12,
20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 78.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8B55FF139F8F81D7 CRC64;
                                                                                                                                                                                           682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 907;
                                                                       chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 6
O9723
ID O972
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AC O972
DE HYPE
DT 01-M
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O97239;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last seque)
O1-DEC-2001 (TrEMBLrel. 19, Last annothypothetical 467.9 kDa protein.
PFC0245C, MAL3P2.18.
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Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 682 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD003142; Hpt; 1.
SMART; SM00260; CheW; 1.
SMART; SM000387; HATPase_C; 1.
SMART; SM00073; HPT; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02518; HATPase_c; 1.
Pfam; PF01627; Hpt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                        Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.; Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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  falciparum .";
Nature 400:532-538(1999).
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum (isolate 3D7).
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                               MEDLINE=99376085; PubMed=10448855;
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=36329;
                                                    "The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EELEEEKF -- DERFLVTLLTKVDGEE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDEFEMTVLDQSFEQGYQAYQIEVTLDE--KTLLKAARVFMVFEVLEQVG-EVIKSTPSA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q56310; 1B3Q
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PF02895; H-kinase_dim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      682 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / JCM 9153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75272 MW; 46B6B1EE5BFE7276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CheW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIS_KIN_sig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bact_sens_pr_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATPbind_ATPase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3933 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RA Adams A.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams A.D., Celniker S.E., Lil P.M., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Asibunner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asibunner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asibunner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asibunner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Zhang O., Chen L.S.,
RA Bardon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Bardon R.C., Makter E.G., Helt G., Nelson C.R., Maklos G.L.G.,
RA Bardis J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bescon K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K.D., Delcher A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Deng F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeyama C.,
RA Harris N.L., Muston K.A., Howland T.J., Wei M.-H., Ibeyama C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Kang M., Mattei B., McIntosh T.C., McLeod M.P., McSherson D.L.,
RA McIntov G., Milshna N.V., Mobarry C., Morris J., McShrefi A.,
RA Harlson D.R., Nelson K.A., Nixon K., Dunkon J., McShrefi A.,
RA Harlson D.R., Nelson K.A., Nixon K., Dunkon J., Nelson D.L.,
RA Mang Z.-Y. Wassarman D.A., Weilson M., Skupski M.P., Smith T.,
RA Ra Har
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InterPro; IFR002048; EF-hand.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 3933 AA; 467876 MW; 5144
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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Pred. No. 1e+02;
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Best Local
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Q03650;
01-NOV-1996 (TrEMBLrel. 01, C:
01-NOV-1996 (TrEMBLrel. 21, L:
01-JUN-2002 (TrEMBLrel. 21, L:
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Best Local :
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           SEQUENCE FROM N.A.
                                      Eukaryota; Euglenozoa;
NCBI_TaxID=5702;
                                                               Trypanosoma brucei brucei
                                                                                       CRAM
                                                                                                Cysteine-rich, acidic integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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CG14853.
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01-JUN-2002
01-JUN-2002
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY071572; AAL49194.1; -.
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                            150 --LDKLRAVATSSDSDENYNKSSSPDLALDLHASDVEADVDGDEAGDADEDGDADAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                         61 EELDQEKFVV-----DENFTEN-----YLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                    14 KYTDFDKS-----FKKSSDLDECKKTCFKTEYCYIVFE---DTVNKECYYNVVDG
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23.9%; Pred. No.
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23.9%;
                                               Kinetoplastida; Trypanosomatidae; Trypanosoma.
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Membrane; Transmembrane; Antigen; Endocytosis; Signal; Repeat;
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EMBL; M61131; AAA30170.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=TREU667BUT55;
MEDLINE=90355963; PubMed=1697030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE HUMAN LOW-DENSITY LIPOPROTEIN (LDL) RECEPTORS, ESPECIALLY TO THE HUMAN LOW-DENSITY LIPOPROTEIN (LDL) RECEPTOR (POl1130). CAUTION: CONCERNING THE CONSENSUS SEQUENCE DDCN/DITGDCNET OF THE DODECAPEPTIDE REPEATS: UP FROM AA 316 IT IS UNSURE IF IT IS AMINO ACID N OR D IN POSITION 4 OF THE REPEATS.
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Q20246; (TremBLrel. 01,
Q1-NOV-1996 (TremBLrel. 01,
Q1-NOV-1996 (TremBLrel. 21,
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                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                           F40G12.5
                                                                                                                                                                                                                                                                                                    F40G12.5 protein
                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z77661; CAB01183.1; -.
                                                                                                                                                                                                               Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                       SEQUENCE
                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform
                                                                                                                          interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ESNAEVGTPPADAVHDDFFFDYKNATGYADDCNITGDCNETDDCDITGDCNETDDC--NI 68
        CYYNVVDGEELDQEKF-VVDENFTE--NYLTDCEGKDAGNAAGTGDESDEVD 101
                          EESEDC-----FEKVFLAIISGKHECSK----DYDFLARNLIQRREALTSGKE 72
                                            EEREDCWTFYANRKYTDFDKSFKK-SSDLDECKKTCFKTEYCYIVFE------DTVNKE 52
                                                                                                                PF03236;
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Q9FIW8;
Q1-MAR-2001;
01-MAR-2001;
01-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barale J.C., Candelle D., Attal-Bonnefoy G., Dehoux P., Bonnefoy S., Ridley R., Pereira da Silva L., Langsley G.;
"Plasmodium falciparum AARPI, a giant protein containing repeated motifs rich in asparagine and aspartate residues, is associated withe infected erythrocyte membrane.";
Infect. Immun. 65:3003-3010(1997).
EMBL; Y08926; CAA70130.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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SMART; SM00184; RING; 1.
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Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                     "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned P1 and TAC clones."; DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                                                   Gb|AAF22924.1 (Hypothetical
                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                    AT5G39780
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Yamada K., Banh J.,
Lee J.M., Onodera C.
                             SEQUENCE FROM N.A.
                                                                                                                           Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima
                                                                                                                                          MEDLINE=99087489; PubMed=9872454;
                                                                                                                                                          STRAIN-COLUMBIA;
                                                                                                                                                                      SEQUENCE FROM N.A.
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1 (TrEMBLrel. 16,
2 (TrEMBLrel. 20,
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  Chang C.H., Chang E., Dale J.M., S., Quach H.L., Tang C., Toriumi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75; DB 5;
pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23D0233261C30DBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3844 AA
                                                                                                                                                                                                                                                                                                                                                              606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 3844;
                                                                                                                                                                                                                                               Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dehoux P., Bonnefoy S.,
          Toriumi M., Wu H.C.,
                                                                                                                                                                                                                                  core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is associated with
                      Goldsmith A.D.,
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Best Local
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    01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                        Q9FK41;
                                                      Q9FK41
                                                                                                                                                                                                                                                                                                Comte P.A., Ossipow V., Schibler U.;
"Isolation of PIP, a 160 kDa nucleolar protein that interacts with the activation domain of PAR transcription factors.";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U83590; AAB62878.1;
EMBL; U83590; AAB62878.1;
SEQUENCE 1277 AA; 144675 MW; 43140A2973178792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           Wuarin J., Schibler U.; "Expression of the liver-enriched transcriptional activator protein DBP follows a stringent circadian rhythm."; Cell 63:1257-1266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=91084854; PubMed=2261643;
                                                                                                                   671 GEESEEEDRDKDVDPGFRQQLM---EVLQAGNALGGEEEEEE 709
                                                                                                                                                                                          630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAR interacting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  035821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035821
                                                                                                                                         60 GEELDQE--KFVVDENFTENYLTDCEGKDAGNAAGTGDESDE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein
                                                                                                                                                                                                        1 EEREDCWTFYANRKYTDFD-KSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVD 59
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 DFVDSSQTFTSNDEDGFLSDSDFAETSLKKGQNRKSDN-SGSGSDSEEEEEE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 NYVDGEEL----DQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EEREDCW--TFYANRKYTDFD----KSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYY 55
                                                                                                                                                                                 EDEED----NVVVTDTDEKQLKHGEDADSDS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKTEDLGYSVFHGEDKVKTEDYSVSSFKK------KKIRFLTE-----EDFLESDS-- 147
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د ا
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                                                 PRELIMINARY;
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TIEMBLIEL 05, Created)
(TIEMBLIEL 05, Last sequence update)
(TIEMBLIEL 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         606 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                          30.4%;
                                                                                                                                                                                                                                                       13.0%; Score 74.5; 30.4%; Pred. No. 66;
                                                                                                                                                                                                                                                                                              144675 MW; 43140A2973178792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71043 MW; 5F02E244E59FC15D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%; Score 74.5;
27.7%; Pred. No. 29;
      16, Created)
16, Last seq
Last sequence update)
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                                                 PRT;
                                                                                                                                                                                                                                            Mismatches
                                              596 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1277 AA
                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 606;
                                                                                                                                                                                                                                    37; Indels
                                                                                                                                                                            -----EDSKNSESDVDSED 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Indels
                                                                                                                                                                                                                                                                  Length 1277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae; Rattus
                                                                                                                                                                                                                                        25;
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                 Query Match
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           InterPro; IPR002052; NULLINGMITERASE.
PRINTS; PR00507; N12N6MTFRASE.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                        Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Yugt R., Palmer N., Adams M.D., Gocayne J.D., Weddman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                          InterPro; IPR002296; N12N6_mtfrase.
InterPro; IPR002052; N6_Mtase.
                                                                                                                                                                                                                                         TIGR; BBH09;
                                                                                                                                                                                                                                                                                                    Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                  "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   050667;
01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                     Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid 1p28-3.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein BBH09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                050667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned pl and TAC clones.";
DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01344; Kelch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 TLDDLYSLNLSKLDEWKCIIPTTETEWVEVSDDEEGDEDDDEDDSEDEGNSEESDDEDDD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 NRRWSDKSKALQGAKTRLDPQVSVSEEVVKPCGRINSCMVVGKDTLYIYGGMMEIKDKEV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similarity to unknown protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=COLUMBIA;
MEDLINE=98403884; PubMed=9734815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 NRKYTDFDKSFK-----KSSDLDECKKTCFKTEYCYIVFEDTV-----NKEC 53
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                                                                                                                                                                                                                                                             AE000784; AAC66000.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35210 / B31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68483 MW; 8865D3CAD873CBD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.9%;
Score 74;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 10; Length 596; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1278 AA.
  DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Indels
Length 1278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E.K., Gwinn M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
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GenCore version
Copyright (c) 1993 - 2003
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Compugen Ltd.
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Command line parameters:

-MODEL-frame+\_p2n.model -DEV=xlh
-Q-\_Cgn2\_1/USPTO\_spool/US99936737/runat\_14022003\_100733\_2299/app\_query.fasta\_1.263
-Q-\_Cgn2\_1/USPTO\_spool/US99936737/runat\_14022003\_100733\_2299/app\_query.fasta\_1.263
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE-pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=bto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09936737\_eGGN 1\_1\_1349\_@runat\_14022003\_100733\_2299 -NCPU=6 -ICPU=3
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPDEXT=0.5 -FGAPDP=6 -FGAPEXT=7 Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Title: Perfect score: Run on: OM protein - nucleic search, Scoring table: Database : Post-processing: Minimum Match 0% -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Xgapop 10.0 , Ygapop 10.0 , Fgapop 6.0 , Delop 6.0 , I US-09-936-737A-2 573 February 25, 2003, 02:33:51; Search time 1946 Seconds (without alignments) 857.212 Million cell updates/sec BLOSUM62 16154066 seqs, 8097743376 residues Maximum Match 100% Listing first 45 summaries EEREDCWTFYANRKYTDFDK..... gb\_est1:\* em\_htc:\* em\_estov:\* em\_esthum:\* em\_estin:\* em\_estro:\* em\_estpl:\* em\_estmu:\* em\_estba:\* gb\_gss:\*
em\_gss\_hum:\*
em\_gss\_inv:\*
em\_gss\_pln:\* gb\_est2:\*
gb\_htc:\*
gb\_est3:\*
gb\_est4:\*
gb\_est5:\* em\_gss\_rod:\* em\_gss\_pro:\* em\_gss\_other:\* em\_gss\_mus:\* em\_gss\_mam:\* em\_gss\_fun:\* em\_gss\_vrt:\* em\_estom:\* em\_estfun:\* using Xgapext Ygapext Fgapext Delext frame\_plus\_p2n model 0.5 7.0 7.0 .GKDAGNAAGTGDESDEVDED 103

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 442<br>443<br>444<br>45  | c 37<br>c 38<br>39   | C<br>334<br>44 33                                     | யயை  | c 28<br>29  | 22325  | 15<br>16<br>17<br>18<br>19<br>20   | 7<br>8<br>9<br>10<br>11<br>12<br>13   | 5<br>5<br>5<br>5<br>6<br>7<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8 | Result      |
|--|--|---|--|---|--|--|---|--|-------------|
| 75.5<br>75.5<br>75.5<br>75.5<br>75.5   | 76<br>76<br>76   | 79<br>78<br>78  | 9. 8   | 82<br>82<br>80.5  | 0 8 8 8 8 8  | 3  | 0 & & & & & & & & & & & & & & & & & & &   | 84.5<br>83<br>82<br>82<br>82   | i ii        |
| 13.2<br>13.2<br>13.2<br>13.2   |  | $\omega \omega \omega$                                | -ωω-   | 444   | .444.  |  | 144.<br>144.<br>144.<br>144.<br>133.  | 44444  | Query       |
| 473<br>478<br>478<br>526<br>640  | 410<br>663<br>721  | 470<br>566<br>947                                     | 499<br>656<br>1058                                 | 706<br>723<br>594   | 663<br>672<br>687  | 5507<br>500<br>620<br>648  | 496<br>541<br>561<br>561<br>561   | 504<br>704<br>462<br>470<br>484<br>493   | Length      |
| 12<br>13<br>17<br>10   | 17   | 13<br>17  | 12<br>17   | 1233  | 10210  | 12<br>12<br>12<br>12   | 12<br>12<br>12<br>12<br>12<br>12  | 10<br>17<br>12<br>12<br>12   | DB          |
| BG08681<br>B1174761<br>AQ701970<br>BJ122797<br>BB645658                                | AA5499//<br>BH316991<br>AQ621585<br>AL726177                       | BG138190<br>BJ101346<br>AZ676398                      | BG138662<br>BF708357<br>CNS05MJS                   | B1933236<br>B1933320<br>B1933312<br>BG138008                                | AW738268<br>BG137992<br>BG136406<br>AW738284                         | BG139637<br>BG139637<br>BG136116<br>AW738722<br>AW738016<br>BG140407<br>BG136420 | BG139798 BG13645 AW737851 BG139905 BG139907 BG138707 BG139936 BG140418  | BE581359 AQ643182 BG141291 BG147845 BG141201 BG141314  | ID          |
| G086881 H3131C<br>I174761 OSTF05<br>Q701970 HS_539<br>J122797 BJ1227<br>B645658 BB6456 | 16991 CH230-12<br>16991 CH230-12<br>51585 Sheared<br>6177 AL726177 | 138190 EST4/863<br>101346 BJ101346<br>676398 ENTJQ511 | 38662 EST47910<br>08357 A1200_LE<br>44161 Tetraodo | 193320 EST55310<br>1933320 EST55320<br>1933312 EST55320<br>G138008 EST47845 | 38268 EST33969<br>37992 EST47843<br>36406 EST47684<br>38284 EST33971 | EST47999<br>EST47655<br>EST34014<br>EST29673<br>EST48084<br>EST47686             | 9798<br>6045<br>9905<br>87094<br>EE<br>9936<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE<br>FE | kq49g04.<br>RPC193-E<br>RST48173<br>EST47828<br>EST47828<br>EST48164   | Description |

## ALIGNMENTS

| RESULT 1   |   |
|------------|---|
| BE581359   |   |
| LOCUS      | BE581359 504 bp mRNA linear EST 09-MAY-2001                               |
| DEFINITION | kq49g04.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5', mRNA            |
|            | sequence.   |
| ACCESSION  | BE581359  |
| VERSION    | BE581359.1 GI:9832301   |
| KEYWORDS   | EST.  |
| SOURCE     | Strongyloides stercoralis.  |
| ORGANISM   | ORGANISM Strongyloides stercoralis  |
|            | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;                    |
|            | Panagrolaimoidea; Strongyloididae; Strongyloides.                         |
| REFERENCE  | 1 (bases 1 to 504)  |
| AUTHORS    | McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T. |
|            | , Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y. |

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VERSION
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                                                                                                                                                                                                                                                    AQ643182
                                                                                                                                                                                                                                                                              RESULT 2
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                                                                                                                                                                                                                                                                                                                              AACAATTAAAAATCGTTGTGTCTTTTATTAT 469
                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAGAATGTATTAAACAATGTTATGGAAATCATTTTTGTTATTCAATTTACTACGATGA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uAspGluCysLysThrCysPheLysThrGluTyrCysTyr---IleValPheGluAs 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheTyrAlaAsnArgLysTyrThr-AspPheAspLysSerPheLysLysSerSerAspLe
                                                                                                                                                                                                                                                                                                                                                                             pThrValAsnLysGluCys-----TyrTyr 55
                                            Trypanosoma brucei
Trypanosoma
                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                       Trypanosoma brucei.
                                                                                                                           AQ643182.1 GI:5119892
                                                                                                                                                                        RPC193-EcoRI-6L8.TJ RPC193-EcoRI Trypanosoma brucei genomic clone RPC193-EcoRI-6L8, DNA sequence.
                                                                                                                                                                                                                            AQ643182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIAID, NIH (tnutman@nih.gov). DNA Sequencing l
University Genome Sequencing Center St. Louis.
High quality sequence stop: 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Washington Univ. Nematode EST Project, 1999 
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         experimentally infected with larvae originally isolated from experimentally infected dogs. cDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the EcoRI site to the XhOI site. The library has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-1700)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="XL-I Blue MRF' (Stratagene)"
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
ECORI; Site_2: XhoI; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Strongyloides stercoralis" /strain="Rhabditiform larvae obtained from /db_xref="taxon:6248"
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54.90%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
223 AACACAGCAGCAGGAACAGGAGAGACAAGTACAGGGGTAGAT 264
                                                                                                                                                                                                                                                                                                   130
                       88 GlyAsnAlaAlaGlyThrGlyAspGluSerAspGluValAsp 101
                                                                                                                                                   71
                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                           31 CysLysThrCysPheLysThrGluTyrCysTyrIleValPheGluAspThrValAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                  11 AlaAsnArgLysTyrThrAspPheAspLysSerPheLysLysSerSerAspLeuAspGlu 30
                                                                                           GATGAGAATGCAACTGACAAAAGCAAAGGGGACTGCAAACCTAAAGAAGAAGAAAAAGACA 222
                                                                                                                                           AspGluAsnPheThrGluAsnTyrLeuThrAspCysGluGlyLysAsp-----Ala
                                                                                                                                                                                                                                            LysGluCysTyrTyrAsnValValAspGlyGluGluLeuAspGlnGluLysPheValVal 70
                                                                                                                                                                                                                                                                                                   TGCAAA----
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujil, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
Library for gene discovery and sequence-ready map construction
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences :
page: http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bohui Zhao in Pieter de Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
brucei TREU927/4 GUTat 10.1 agarose embedded DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI93-EcoRI"
/note="Vector: pBACe3.6; Site_1: Eco RI; Site_2: Eco RI;
Constructed for The Institute for Genomic Research by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="TREU927/4 GU
/db_xref="taxon:5691"
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27.66%
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BG141291
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Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from wild tomato (L. pennellii) pollen
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BG141291.1 GI:12641480
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
BG137845 #INA EST478287 wild tomato pollen Lycopersicon cLpP7D15 5' sequence, mRNA sequence. BG137845 #EG137845.1 GI:12638033
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/tissue_type="pollen"
/dev_stage="pollen collected from open flowers"
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/clone="cLPP20L16"
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Lycopersicon pennellii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from wild tomato (L. pennellii) pollen
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Lycopersicon pennellii
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Unpublished (2001)
             Hansen,C., Ronning,C. and Tanksley,S. Generation of ESTs from wild tomato (L. pennellii) pollen
                                                   van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
                                                                                                                   Lycopersicon pennellii Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Lycopersicon pennellii
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Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from wild tomato (L. pennellii) pollen
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/tissue_type="pollen"
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/clone="cLPP20I10"
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/lab_host="SOLR"
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/cultivar="TA56"
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         Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
                                                                                                                                       van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tanksley, S.
Generation of ESTs from wild tomato (L. pennellii) pollen
                                                                                                            Contact: CUGI
                                                                                                                              Unpublished (2001)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Clemson, SC 29634, USA
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/tissue_type="pollen"
/dev_stage="pollen collected from open flowers"
/lab_host="SOLR"
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EST476487 wild tomato pollen Lycopersicon pennellii cDNA clone
cLPP1020 5' sequence, mRNA sequence.
BG136045
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Generation of ESTs from wild tomato (L. pennellii) pollen
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/dev_stage="pollen collected from open flowers"
/dev_stage="pollen"
/lab_host="SOLR"
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|Cultivar="TA56"
|/db_xref="taxon:28526"
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                                                                                                                                                                                                                                                        Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                    van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue, anthesis
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                                                                          University"
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/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                             100 Jordan Hall, Člemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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EST480347 wild tomato pollen Lycopersicon pennellii cDNA clone
CLPP14N18 5' sequence, mRNA sequence.
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                                    /note-"Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: xho1; Pollen was collected from open flowers from L.pennellii TA56, and stored at -80 C until library
                                                                                                                     /clone_lib="wild tomato pollen"
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/cultivar="TA56"
                                                                                                              /lab_host="SOLR"
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                                                                                                                                                                                                   /clone="cLPP14N18"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: CUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/clone="cLpp1J21"
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Generation of ESTs from wild tomato (L. pennellii) pollen
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/tissue_type="pollen"
/dev_stage="pollen collected from open flowers"
/lab_host="SOLR"
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Generation of ESTs from wild tomato (L. pennellii) pollen
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
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BG37480860 wild tomato pollen Lycopersicon pennellii cDNA clone CLPP17M7 5' sequence, mRNA sequence.
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/tissue_type="pollen"
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/clone="cLPP17M7"
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                                                                            352 ATTGATTCAATGAAAAAGGCAACACAAGATGTT-----AAAGAACTAAATTATTAC 402
                                                                                                                                                                                                                                         238 AAGACACAAGATTTTATCAAAAATGTAATTGATAAAAGATTGGCTTCAAGTGCACCAATA 297
                                      67 LysPheValValAspGluAsnPheThrGluAsnTyrLeuThrAspCys 82
                                                                                                                                                             298 GATCATTATAAGAAAGATTGTTTTAAAACA-----TGCAAAGAGGTGTATGAAGATGCA 351
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Generation of ESTs from wild tomato (L. pennellii) pollen
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561 bp mRNA linear EST 31-JAN-
EST480863 wild tomato pollen Lycopersicon pennellii cDNA clone
CLPP17M13 5' sequence, mRNA sequence.
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